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Breeding orchardgrass for satisfactory Oregon seed yield combined with high Iowa forage yield and quality

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Breeding orchardgrass for satisfactory Oregon seed yield combined with high Iowa forage yield and quality

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DEDICATION

To the memory of my mother.

--Roy Luedtke

INTRODUCTION

Orchardgrass, Dactylis glomerata L., is a cool-season perennial forage grass which has been successfully used in temperate regions of the world. It is well-suited for pasture and hay, either in mixtures with legumes or in pure stands. Desirable attributes of orchardgrass are ease of establishment, ability to recover rapidly after cutting or grazing, production of satisfactory second and third growths, shade tolerance, and excellent nutritive value and palatability when properly managed.

Improvement of forage yield, quality, and disease resistance are major objectives of most orchardgrass breeding programs. Breeding for improved seed production is also an important objective because new cultivars must be satisfactory in seed production in the Willamette Valley of Oregon where 98% of the orchardgrass seed produced in the United States is grown (Youngberg, 1980). Seed producers will not grow cultivars that are relatively low in seed yield unless the price received for the seed compensates for the lower yield. Therefore, cultivars selected for adaptation and forage characteristics in the midwest or eastern U.S. must be selected for satisfactory seed production in Oregon.

The objectives of this study were: (1) to evaluate elite orchardgrass breeding material for seed production in the Willamette Valley of Oregon and near Ames, Iowa; (2) to determine the degree to which seed yields in Iowa predict seed yields in Oregon; (3) to determine the correlation between parent clones and polycross progenies for seed

production and related traits in both states and between states; (4) to determine traits which could be used in Iowa to select among clones or individual plants for satisfactory seed production in Oregon; and (5) to study relationships between seed and forage traits.

REVIEW OF LITERATURE

Nature of Orchardgrass and Breeding Behavior

Studies on the distribution of orchardgrass in conjunction with chromosome counts began in the 1930s. Levan (1930) found that both cultivated and wild forms of subspecies glomerata in northern Europe were tetraploid. Müntzing (1937) showed that subsp. aschersoniana Graebner was diploid, and he hypothesized that tetraploid D. glomerata originated by chromosome doubling of aschersoniana. He later changed his opinion that D. aschersoniana was the progenitor of D. glomerata, but stated that D. aschersoniana must be very closely related to the original form of glomerata (Borrill, 1977). During subsequent years, numerous workers proposed various hypotheses. Clausen et al. (1945) and Stebbins (1947) proposed the possibility of hybrid origin with the participation of an additional diploid form or forms. In 1948, Myers reported finding a diploid in Iran, subsp. woronowii Ovczinn, which crossed with aschersoniana and the resulting F_1 resembled many plants of the glomerata type found in northern Europe. The cytogeographic survey of the genus was accelerated by extensive plant collections made in the Mediterranean region in the early 1950s by Stebbins (Borrill, 1977). Stebbins and Zohary (1959) published results based on his collections. They concluded that the diploid subspecies of Dactylis were generally crossable and able to exchange genes readily at the diploid level. They felt that cultivated tetraploid D. glomerata was formed by chromosome doubling of hybrids among the various diploid subspecies.

Of the autopolyploid forage grasses, orchardgrass is cytologically the most investigated crop. In meiosis, it behaves as an autotetraploid (2n=28) and forms an average of three to four quadrivalents per cell (Müntzing, 1933; Morrison and Rajhathy, 1960). Jones (1962) found an average of 2.77 quadrivalents per cell along with rare occurrences of trivalents and univalents. McCollum (1958) found an average of 3.31 quadrivalents per cell in seven natural subspecies of tetraploid Dactylis. In the same study, using natural and induced forms of tetraploid Dactylis, he found no evidence for preferential pairing, and consequently no support for the hypothesis of structural differentiation of chromosomes between the diploid subspecies.

The inheritance of a few qualitative characters has been studied. Most studies have involved chlorophyll deficiencies. Myers (1941) found that the frequency of albino seedlings in segregating progenies could be explained on the basis of tetrasomic inheritance and random chromosome segregation. Brix and Quadt (1953) studied the same character as Myers and came up with similar results. Cuany and Kalton (1960), however, could not explain their results by any specific model. They concluded that a combination of tetrasomic and disomic inheritance, probably caused by preferential pairing, was working in their material.

Similar to most perennial forage species, orchardgrass is highly cross-pollinated and variable in self-fertility. Stapledon (1931) found that the degree of self-fertility varied greatly among individual plants of orchardgrass. He found that plants ranged from completely self-sterile to completely self-fertile. He also found that, on the average,

orchardgrass plants were about half as vigorous vegetatively when derived from selfing as when derived from hybridization. Schultz (1941) found that S_1 and S_2 plants of orchardgrass yielded, on the average, only 60 and 43%, respectively, as much as their parental clones. Myers (1942) reported a 63% decrease in selfed seed set from one generation of selfing. Kalton et al. (1952) found that 55 S_1 progenies of orchardgrass were approximately 21% lower than their parents in average vigor. They also found a progressive decrease in vigor from the S_1 to the S_2 generation. They concluded it would be extremely difficult to isolate superior segregates during inbreeding because of the depression in vigor and seed set. In general, the degree of self-fertility has been sufficient to enable breeders to practice limited inbreeding (Leffel et al., 1954).

Kalton and Leffel (1955) studied combining ability among 11 non-inbred clones of orchardgrass. They found that variances attributable to general combining ability were greater than those for specific combing ability for spring vigor, bloom date, panicle production, and forage yield. Disease score was the only trait exhibiting a significant amount of specific combining ability. Knight (1966) reported results which supported Kalton and Leffel's work. Oldemeyer and Hanson (1955) studied combining ability in orchardgrass using progenies obtained from wide polycrosses, restricted polycrosses, and single crosses. They reported that the specific combining ability exhibited among single crosses would be of importance when only a few parents are to be combined into a synthetic variety. Along this line, Christie (1973) and Christie and Krakar

(1980) reported yield increases utilizing single- and double-cross hybrids of orchardgrass. In the latter paper, they reported that certain hybrids did not decline in yield when advanced to the F_2, but went on to say that due to present seed production problems, hybrid cultivars appear to be impractical. In summary, the literature indicates that four to eight unrelated parents high in general combining ability for seed and forage yield should be used to form a synthetic (Bowley and Christie, 1981).

Use of the Polycross Method in Grass Breeding

In 1940, Frandsen described a method for breeding timothy (Phleum pratense L.) that involved testing a group of selections for general combining ability in such a way that variation in male parentage was not a factor in progeny performance. He did not name the procedure. Two years later, Tysdal et al. (1942) developed a similar procedure for use in breeding alfalfa (Medicago sativa L.) and coined the term "polycross". In 1947, Wellensiek described a general method for breeding cross-pollinated species. A major portion of his procedure was termed "mass test crossing". The methods developed independently by these researchers were similar in principle and later became known as the polycross test. The polycross method involves the production of seed for progeny testing in such a way that each parental genotype has an equal opportunity of being pollinated by all other genotypes. Random mating is probably never attained, but it is sought by replication, randomization, experimental design, and selection for similar maturity. One important requirement

of the polycross test is that the parents must be capable of being propagated vegetatively so that they may be kept until the progenies have been evaluated.

Kalton (1959) stated that polycross mating blocks have a significant role in breeding programs which deal with cross-pollinated forage crops. He went on to say that they may be used for: (1) recombining clonal selections or lines into new experimental synthetics; (2) production of polycross seed for progeny testing; (3) production of breeder's seed of new varieties; and (4) intercrossing selections in a recurrent selection program. Oldemeyer and Hanson (1955) along with Kalton and Leffel (1955) utilized polycross progenies for evaluating combining ability in orchardgrass. Miller and Carlson (1982) used polycross progenies for testing orchardgrass clones for resistance to rust (Puccinia graminis Pers.). They also utilized the polycross mating block to recombine plants selected on the basis of phenotypic and phenotypic-genotypic performance during three cycles of selection for rust resistance. Hovin et al. (1966) used polycross progenies of selections from adapted experimental breeding strains to study nonflowering plants of orchardgrass. Using a polycross mating block, they formulated three 4-clone experimental synthetics with different inductive requirements for flowering. Christie (1977) evaluated one cycle of phenotypic selection for in vitro digestibility in orchardgrass using two groups of polycross progenies. As these examples indicate, polycross mating blocks have played an important role in orchardgrass breeding programs.

Breeders resort to progeny testing when the heritability of a particular phenotypic expression is low. Morley and Heinrichs (1960) estimated that heritability has to be as low as 10% before the inclusion of a progeny test will result in greater annual improvement than phenotypic selection. Similar results were found by Miller and Carlson (1982) when working with rust resistance in orchardgrass. They found one cycle of phenotypic-genotypic selection achieved the same level of rust resistance and required the same length of time as two cycles of phenotypic selection. Hill et al. (1971) evaluated 67 alfalfa clones and their polycross progenies for hay, seed, and chaff yields. Expected genetic gains from selection on the basis of clonal and polycross progeny-test performance were compared for each of the characters. They found the relative effectiveness of the two methods varied with heritability of the trait and the selection intensity permitted. In general, the polycross progeny test favored traits with low heritability.

Results of research on randomness of mating in polycrosses have been reported in the literature. Grunder and Dermanis (1952) looked at proximity of clones as a factor in the frequency with which a plant served as a pollinator in a polycross. They found that pollinator plants of orchardgrass had little effect at distances greater than 1.4 meters. Wit (1952) estimated that in a polycross of perennial ryegrass (Lolium perenne L.) parent clones were fertilized, on the average, 40% of the time by the two adjacent clones and 74% of the time by the three neighboring clones on each side. Wassom and Kalton (1958) found similarity in forage yield of separate replicate entries from a polycross of

orchardgrass, indicating random pollination. However, for panicle number, six of nine variance ratios were significant, indicating nonrandom pollination for that character. Knowles (1969), working with smooth bromegrass (Bromus inermis Leyss.), found that the direction of prevailing winds had an impact on randomness of mating. He found that plants upwind served more frequently as pollinators for adjacent plants downwind. Carlson (1971), who used the alborviridis gene as a genetic marker in a polycross of orchardgrass, found that random mating did not occur. He went on to say that although the results raise a question about the use of the polycross test for evaluation of parents, the test should not be discarded until it is determined whether non-random mating is a serious factor in evaluation for quantitatively inherited traits.

Tysdal and Crandall (1948) demonstrated the need for selecting parents of high combining ability to produce high yielding alfalfa synthetics. They produced two synthetics, one with high combining parents and one with low combining parents. The former yielded 29% more forage in the first generation than did the low combining synthetic. They concluded that as long as there was considerable genetic variability among clones in a polycross nursery the polycross test should measure general combining ability efficiently. Murphy (1952) compared the performance of parental clones with that of polycross and selfed progenies from three different species of grasses. He used drilled, broadcast, and spaced-plantings for progeny evaluation. Significant, positive correlations were obtained between parental and progeny yields regardless of the method of testing or planting. He concluded that any of the

methods tested could be used in selecting parents for high yield potential. Oldemeyer and Hanson (1955) studied combining ability in orchardgrass by evaluating single-cross and polycross progenies of 38 parents. They found that the average forage yields of single-cross progenies from the respective parents were significantly correlated with parental and polycross yields. Wassom and Kalton (1958) stated that the use of single crosses for testing clones is laborious, costly, and not practical on a large scale. Timothy et al. (1959) found fair agreement between polycross progeny performance and average single-cross performance as tests for combining ability in smooth bromegrass. Frakes and Matheson (1973) compared various methods of progeny testing for forage yield in tall fescue (Festuca arundinacea Schreb.). Single cross, open-pollination, polycross, and F_2 progenies all identified the same high and low performing genotypes. They suggested the use of open-pollination or polycross progeny since they can be obtained in less time and at a lower cost than a diallel set of progeny.

In summary, the polycross test is aimed at investigating the general combining ability of a group of individuals. It includes an easy practical way of producing seed for a reliable progeny test.

Breeding for Seed and Forage Characteristics

Agronomic traits influencing seed yield

Seed yield of grasses such as orchardgrass is the product of number of panicles per unit area and seed yield per panicle. The latter characteristic is determined by number of seeds per panicle and weight

per seed. Number of seeds/panicle, in turn, is affected by panicle size, or number of florets, and seed set or fertility. To assess the possibility of genetic improvement in seed yield, it is necessary to determine the extent and nature of genetic variation, genotype x environment interactions, interrelationships, and heritability of seed production characters. Relatively little research has been conducted on breeding for seed yield in orchardgrass, but a number of relevant studies have been conducted on similar grasses.

The heritability of panicle number and its relationship to seed yield has been studied in several grasses. Kalton et al. (1955) found a low nonsignificant correlation of 0.30 between panicle number and seed yield in a clonal test of orchardgrass. Nielson and Kalton (1959), on the other hand, found panicle number along with fertility to be the primary components of seed yield in smooth bromegrass. They reported genetic correlations of 0.80 and 0.69 between seed yield and panicle number in each of two years of testing. In crested wheatgrass, Schaaf (1976) obtained positive phenotypic and genotypic correlations of 0.70 and 0.39, respectively, between panicle number per plant and seed yield. He also reported a negative association between panicle number per plant and seed weight. Bean (1972) reported broad-sense heritability estimates for panicle number in tall fescue and timothy of 0.28 and 0.08, respectively. The heritability estimate for timothy was low because of a large genotype x year interaction. Oram (1982) obtained a broad-sense heritability estimate of 0.48 for panicle number in Phalaris aquatica L., along with a genetic correlation of 0.58 between panicle number and seed yield. Nguyen and Sleper (1983) reported broad- and

narrow-sense heritability estimates of 0.77 and 0.92, respectively, for panicle number in tall fescue.

Researchers have reported a positive relationship between seed yield per panicle and seed yield. In tall fescue, five-panicle gross weight and five-panicle clean seed weight accounted for a high proportion of the total variation in seed yield per plant (Frakes, 1980). In crested wheatgrass (Agropyron desertorum (Fisch. ex Link) Schult.), Dewey and Lu (1959) found positive phenotypic and genotypic correlations of 0.58 and 0.62, respectively, between seed weight per spike and seed yield per plant. Trupp and Slinkard (1965) found positive phenotypic and genotypic correlations between seed weight per spike and percentage seed set in intermediate wheatgrass (Agropyron intermedium (Host) Beauv.). Nguyen and Sleper (1983) estimated broad- and narrow-sense heritabilities of 0.61 and 0.50, respectively, for clean seed weight per panicle in tall fescue.

Panicle size, as reflected by panicle length, may be an important component of seed yield per panicle, however, very little attention has been given to this character in forage grasses. Stoddert (1959) found that earlier maturing strains of timothy had longer panicles and higher seed yields. Jessen (1981), however, found no association between panicle length and seed yield in smooth bromegrass. Panicle length also was not correlated with seed weight, fertility index, and seed number per panicle. Conversely, Nguyen and Sleper (1983) found significant correlations of -0.95, -0.82, and -0.62 between panicle length

and maturity score, panicle number, and seed yield, respectively, in tall fescue. They found no association between panicle length and seed weight. Bugge (1981) found that longer spikes of perennial ryegrass had a greater number of spikelets per spike. He found no association, however, between spike length and florets per spikelet, seed yield per spike, and seed yield per plant.

Much of the variation observed in seed yield per inflorescence or plant of perennial forage grasses can be attributed to variation in fertility or seed set. Nilsson (1934) reported positive correlations between overall plant vigor and fertility and between plant height and fertility in various forage grasses. Leffel et al. (1954) found a positive association between cross-fertility and seed yields of parental orchardgrass clones. Lowe and Murphy (1955) studied seed setting among open-pollinated clones of smooth bromegrass and found a significant correlation of 0.94 between fertility percentage and seed yield per plant. Jessen (1981) also found a significant correlation of 0.85 between fertility index and seed yield in smooth bromegrass. Dewey and Lu (1959) through path-coefficient analysis of seed yield in crested wheatgrass found fertility and plant size to be the most important components of seed yield. In smooth bromegrass, Christie and Kalton (1960) found that fertility was significantly correlated with seed weight and seed yield ($r=0.58$ and 0.65, respectively). Slinkard (1965) found fertility to be a major component of seed yield in intermediate wheatgrass. He reported that narrow-sense heritability estimates for fertility ranged

from 0.53 to 0.57 depending on whether the parents and topcross progenies were grown in the same or different years. Bean (1972) reported broad-sense heritability estimates of 0.51 and 0.36 for fertility in tall fescue and timothy, respectively. In summary, fertility is a component of major importance in determining seed yield potential of forage species.

A major determinant of harvestable seed in perennial forage grasses is seed weight. Stapledon (1928) found that earlier-maturing strains of orchardgrass tended to have larger seeds than later-maturing strains. Most of the available information on the association between seed weight and seed yield comes from studies on other forage species. Christie and Kalton (1960) found seed weight, fertility index, and seed yield all positively associated in smooth bromegrass. Trupp and Carlson (1971) evaluated three cycles of recurrent phenotypic selection for high seed weight in smooth bromegrass. They found no appreciable change in seed set, seed yield, and forage yield during cycles of selection, however, the three cycles averaged lower in fertility index than five varieties. They were successful in increasing initial seedling vigor by selection for high seed weight. Acikgoz and Tekeli (1980) found seed weight and seeds per panicle the primary components of seed yield in smooth bromegrass. In contrast, Jessen (1981) found seed weight to be negatively associated with seed yield, seed number per panicle, and fertility index in smooth bromegrass. Dewey and Lu (1959) found no association between seed weight and seed yield in crested wheatgrass. They also found genotypic correlations of -0.71 and 0.53 between seed

weight and fertility, and between seed weight and plant height, respectively. Schaaf and Rogler (1963), also working with crested wheatgrass, found similar results. A strong negative correlation was obtained between seed yield and seed weight.

Heritability of seed weight has been studied in several species. Christie and Kalton (1960) obtained a significant parent-progeny correlation of 0.56 for seed weight in smooth bromegrass, indicating it is somewhat heritable. Bean (1972) found fairly high broad-sense heritabilities of 0.74 and 0.83 for seed weight in tall fescue and timothy, respectively. Nguyen and Sleper (1983) reported broad- and narrow-sense heritability estimates of 0.89 and 0.19, respectively, for seed weight in tall fescue. Hearn and Holt (1969) found low parent-progeny correlations and unfavorable heritability estimates for seed weight in kleingrass (Panicum coloratum Walt.). Oram (1982) reported a narrow-sense heritability estimate of 0.78 in Phalaris aquatica L. for seed weight. As seen from the above discussion, heritability estimates are frequently favorable and selection for high seed weight should result in improvement.

Maturity seems to be a character which has a large influence on seed yield and its components in orchardgrass. As mentioned previously, Stapledon (1928) found that earlier-maturing strains of orchardgrass had larger seeds and fewer barren tillers than late maturing strains. Carlson and Moll (1962) also found that late maturing strains of orchardgrass were generally less productive in the spring and produced fewer panicles. Kalton et al. (1955) found a significant correlation

of -0.51 between bloom date and panicle number in a clonal nursery of orchardgrass. However, he found no association between bloom date and clonal seed yield in his material. Tomov and Blazhev (1975), on the other hand, examined orchardgrass clones of diverse origin and found that high seed yield was obtained mainly from early-maturing plants bearing few leaves. Stoddert (1959) studied seed development and yield of three varieties of timothy. Within each variety, he found, on the average, a correlation of -0.92 between date of inflorescence emergence and head length. He felt the correlation was strong enough for classifying heads within each variety for maturity based on head length. He found that late maturing heads had lower seed yields and 1000-seed weight than early maturing heads. Christie and Kalton (1960) found similar results in smooth bromegrass. Bloom date was negatively correlated with fertility, seed weight, and seed yield. Leffel et al. (1954) found no association between bloom date and cross-fertility in single-cross and topcross progenies of the same 20 parent clones. Nguyen and Sleper (1983), working with tall fescue, found that early maturing plants had a greater number of panicles with shorter length and higher seed yields. They felt increased seed yield and size could be expected from selection for early maturity. Oram (1982), on the other hand, found no association between anthesis date and seed yield in Phalaris aquatica L. He went on to say that there should be no deleterious correlated responses in date of flowering, herbage yield, or plant height when selecting for higher seed yields in Phalaris.

Maturity is a trait usually thought of as being highly heritable. Kalton et al. (1955) reported significant parent-polycross progeny and parent-topcross progeny correlations of 0.60 and 0.59, respectively, for maturity in orchardgrass. Carlson (1966) found a highly significant parent clone-topcross progeny correlation of 0.82 for bloom date in reed canarygrass (Phalaris arundinacea L.). Nguyen and Sleper (1983) reported broad- and narrow-sense heritability estimates of 0.93 and 0.86, respectively, for maturity in a broad-based population of tall fescue.

Heritable variation in seed yield itself has been reported in several grasses. Ross and Adams (1955) found a significant parent-progeny correlation of 0.67 for seed yield in smooth bromegrass. Similarly, Schaaf and Rogler (1963) obtained a significant parent clone-polycross progeny correlation of 0.54 for seed yield in crested wheatgrass. Carlson (1966) reported a low but significant parent-progeny correlation of 0.30 for seed yield in reed canarygrass. Nguyen and Sleper (1983) obtained broad- and narrow-sense heritability estimates of 0.43 and 0.67, respectively, for seed yield in tall fescue. Kalton et al. (1955) reported a nonsignificant interseasonal correlation coefficient of 0.20 for clonal seed yield in orchardgrass, indicating a large genotype x environment interaction. Burton and DeVane (1953) reported a broad-sense heritability of 0.76 for seed yield among 49 tall fescue clones. Predicted genetic gain from one cycle of selection for seed yield was 61% over the unselected population mean.

This estimate indicated great potential for seed yield improvement, however, it was estimated from the total genetic variance based on a single environment.

Genotype x environment interactions for seed yield and related traits

The quantity and quality of forage produced are the main selection criteria in forage grass breeding, but breeders have recognized that seed yield is the most important trait for the seed producer. Breeding orchardgrass in the United States is complicated by the wide separation of forage and seed production areas. The domestic seed production of most temperate grasses occurs in Oregon, Washington, and Idaho (Youngberg, 1980), while approximately 60% of their usage for forage production occurs in the Midwest (personal communication, S. K. Barnhart, Agronomy Dept., ISU, 1984).

The Willamette Valley of Oregon is the most concentrated area of grass seed production in the Pacific Northwest (Youngberg, 1980). Youngberg reported that, in 1977, Oregon produced all of the United States seed production of annual ryegrass (Lolium multiflorum Lam.), perennial ryegrass (L. perenne L.), red and chewings fescue (Festuca rubra L. and F. rubra subsp. commutata Gaud.) and bentgrass (Agrostis tenuis Sibth.). In addition, 98% of the orchardgrass, 47% of the Kentucky Bluegrass (Poa pratensis L.) and 6% of the tall fescue was produced in Oregon.

Production of orchardgrass seed in Oregon is relatively new. Rampton and Jackson (1969) reported that the area devoted to orchardgrass seed production in Oregon increased from about 49 hectares in 1957, to

approximately 3,240 hectares in 1966. Youngberg (1980) reported that, in 1977, 4,450 hectares of orchardgrass seed were harvested in Oregon, with an average yield of 820 kg/ha.

The concentration of forage grass seed production in the Pacific Northwest emphasizes the need for determining seed yield performance in that area. Little information is available on seed yield and related traits of orchardgrass in the Pacific Northwest. The cultivar "Sterling" is a synthetic variety of orchardgrass selected for high seed yield in Iowa (Kalton and Carlson, 1966). Average annual seed yields of the varieties "Sterling," "Potomac," "Pennlate," and "Latar" were, respectively, 326, 218, 263, and 266 kg/ha when grown in Iowa tests from 1957-1964 (Carlson et al., 1962). In Oregon, these same varieties yielded, respectively, 562, 644, 646, and 525 kg/ha during 1958-1960 (Rampton, 1963). Hill and Hovin (1964) felt variaton in seed set was one of the reasons for year-to-year and location-to-location variation in seed yield of orchardgrass and two other perennial grasses. They tried to relate meiotic irregularities of the three cool-season grasses with variations in seed set. They used the number of micronuclei found in quartets as an assay for determination of meiotic irregularities. Results from the study showed that micronuclei determinations did not differ among locations in the western United States for seven of eight orchardgrass clones. However, significant differences were obtained in percentage seed set among clones as well as among locations. They concluded that meiotic irregularities did not affect seed set in their material.

Lessman and Kalton (1965) evaluated topcross progenies of smooth bromegrass clones for three years at two locations in Iowa. Significant

correlations between locations for seed yield, seed weight, fertility index, and panicle number were 0.80, 0.85, 0.56, and 0.52, respectively. They also reported parent-progeny correlations of 0.42, 0.49, and 0.59, respectively, for seed yield, fertility index, and seed weight. Over a two-year period, Buckner et al. (1972) examined tall fescue clones in Washington and Kentucky. Results revealed that clones differed at both locations for time of panicle emergence, date of anthesis, percentage fertile florets, percentage fertile pollen, number of panicles per plant, seed yield per plant, and 100-seed weight. They found correlations of 0.67 and 0.72 between locations each year, respectively, for seed yield.

Rincker et al. (1977) studied the effect of two diverse environments on seed production characteristics of the parent clones of "Vantage" reed canarygrass. Eight characteristics were measured on each of the six parent clones grown at Prosser, Washington, and near Ames, Iowa. Similarities among location-year combinations in rankings of clones were evident for each trait. They found that the range in means was greater at Prosser for anthesis, panicle number, florets per panicle, and percentage seed set. Overall means at Ames and Prosser were, respectively, 213 and 280 panicles per plant, 645 and 896 florets per panicle, 79 and 70 percent seed set, 88 and 92 mg/100 seeds, and 42 and 102 grams of seed per plant. In a follow-up paper, Rincker and Carlson (1983) reported that polycross progeny performance was positively correlated with parental clone performance for anthesis date, plant height, and panicle number.

Correlations between forage and seed yield

As mentioned earlier, the quantity and quality of the forage produced are the main traits of interest in the forage producing areas. Several researchers have reported results on relationships between forage and seed production. Kalton et al. (1955) reported a low nonsignificant correlation of 0.16 between forage and seed yield of 20 orchardgrass clones. Burton and DeVane (1953) found no correlation between forage and seed yields of tall fescue clones. In their study, plants producing high seed yields were only average in forage production and plants that produced the most forage were below average in seed production. Ross and Adams (1955) evaluated parents and various types of progenies of a smooth bromegrass population. They reported no association between seed and forage yields of open-pollinated progenies. They also found no correlation between years for forage yield, indicating a large genotype x year interaction. Nielson and Kalton (1959) found forage and seed yield positively correlated in smooth bromegrass, but the predictive value was low. Schaaf et al. (1962) also found no association between forage and seed yield in crested wheatgrass, but they did obtain a significant correlation of 0.40 between forage yield and seed weight. Knowles et al. (1970) found no adverse effects on forage production from selection for high seed yield in smooth bromegrass. A low, positive correlation of 0.22 was obtained between seed and forage yield of the polycross progenies.

Breeding for improved forage quality

Improved forage quality is another characteristic breeders strive for in improved synthetics. Tilley and Terry (1963) developed a laboratory procedure for determining dry matter digestibility which simulates the rumen fermentation process. The procedure is known as the *in vitro* dry matter digestibility (IVDMD) technique. The IVDMD values obtained have been highly correlated with *in vivo* digestibility values. Thus, the procedure gives a meaningful measure of digestibility of small forage samples. Christie and Mowat (1968) found a range of 490 to 680 g/kg digestible dry matter among 444 orchardgrass clones with most of the observed variation being attributed to genotypic effects. They also found that IVDMD was negatively associated with maturity and forage yield. Carlson (1974) reported similar results. High IVDMD in spring growth was associated with late maturity and relatively few stems. He also found that leaf diseases, especially rust (*Puccinia graminis* Pers. f. sp. *dactylidis* Guyot et Massinot) reduced IVDMD values in orchardgrass. Edwards et al. (1981) studied effects of rust on digestibility of orchardgrass in more detail and found that sections of leaves from healthy tissue were completely digested except for lignified structures, while sections from diseased leaves showed no apparent digestion of tissues under uredia and only partial digestion of adjacent tissue. They hypothesized that biochemical compounds synthesized by the host, pathogen, or host-pathogen interaction may have been toxic to the rumen microflora.

Christie (1977) practiced one cycle of phenotypic selection for high digestibility in bromegrass and orchardgrass. In spite of a parent-progeny correlation of 0.55 in bromegrass, phenotypic selection for high IVDMD did not result in any improvement over the check cultivar "Saratoga". The polycross progenies of the 10 orchardgrass parents selected for high IVDMD exhibited a range of 683-697 g/kg digestible dry matter. Progenies from the low IVDMD exhibited a range of 673-700 g/kg of digestible dry matter and were not statistically different from the high group. Stratton et al. (1979) evaluated parents and polycross progenies of orchardgrass for IVDMD and related traits. They found early maturity to be negatively correlated with high IVDMD at the time of first harvest, and they suggested it may be difficult to either increase IVDMD or lower fiber content in regrowth without decreasing dry matter yield. Vogel et al. (1981b), on the other hand, found phenotypic selection effective for improving digestibility of switchgrass (Panicum virgatum L.). They improved digestibility without any loss of yield or decrease in protein content.

Berg et al. (1981) working with orchardgrass found that synthetics with relatively few flowering-tillers when grown in the northeastern United States flowered and produced satisfactory seed yields at Prosser, Washington. However, the decrease in flowering-tillers did not improve digestibility percentage of the synthetics. Vogel et al. (1981a) measured height, color, erectness, leafiness, and vigor in indiangrass (Sorghastrum nutans (L.) Nash.) in an attempt to determine associations with yield and quality of forage. Results indicated that vigor,

leafiness scores, and plant height may be useful in selecting for yield. However, none of the five traits were found to be useful in selecting for high IVDMD.

Selection for Seed and Forage Traits

Forage grass breeders have to consider several traits when choosing among selection units. As they make their selections, they usually have a mental picture of how the ideal synthetic should look and perform. This mental picture by the breeder is termed "the art of plant breeding".

To help the breeder, there are three multiple-trait selection methods available (Falconer, 1960): (1) tandem selection, which is simply selecting in turn for each character singly; (2) independent culling levels, in which a breeder selects for all characters at the same time but independently of each other, rejecting all individuals which fail to come up to a predetermined standard for each character no matter what their values are for the other characters; and (3) index selection.

Smith (1936) developed index selection as a means of taking more than one trait into account when making selections in plant breeding. Hazel (1943) extended the principle by outlining methodology to estimate genetic variances and covariances and discussed the incorporation of this information into an index. In order to calculate this index, it is necessary to know: (1) the relative economic importance or worth of each character; (2) the genotypic and phenotypic variances of each character; and (3) the genotypic and phenotypic covariances (or

correlations) between each pair of characters. Robinson et al. (1951) showed how phenotypic and genotypic variances and covariances could be calculated in a cross-pollinating species. They demonstrated the use of these parameters in the construction of a selection index.

Heidhues (1961) and Williams (1962) showed that efficiency of the index may decrease when estimates of population parameters are not determined accurately. This has led to various proposals of other indices which do not require estimates of population parameters. Elston (1963) proposed a multiplicative index which does not require the estimation of population parameters or economic weights. However, this index is not as efficient as one that uses relative economic weights, provided that the weights are assigned correctly (Smith et al., 1981b). Mulamba and Mock (1978) proposed the rank summation index. It is constructed by ranking the phenotypic values for each trait for each member of the breeding population and then simply summing the ranks to give an index value for each member. Pesek and Baker (1969) suggested that breeders would be better able to specify a desired gain rather than an economic weight for a trait. Therefore, the index developed by them used desired gains specified by the breeder rather than economic weights. Crosbie et al. (1980), however, found that the Pesek and Baker index may be inefficient in some situations. It has been found quite often that many of these indices are highly correlated with the Smith-Hazel index (Smith et al., 1981a).

Index selection has been shown to be more efficient when compared to other selection procedures. Robinson et al. (1951) constructed an

index for yield in corn (Zea mays L.) which was predicted to be 30% more efficient than selection for yield alone. Rasmuson (1964) examined three methods for changing the mean number of abdominal and sternopleural bristles in Drosophila melanogaster. Independent culling was superior in increasing bristle number, while index selection was favored for decreasing bristle number. Tandem selection was the least effective of the three methods. Brim et al. (1959) compared indices which included up to six traits for improving economic value in two populations of soybeans (Glycine max Merrill). In both populations, an index of two simply-inherited traits, seed weight and fruiting period, was expected to produce gains nearly as high or higher than those from direct selections for yield of grain, protein, or oil. Elgin et al. (1970) compared tandem, modified independent culling levels, estimated index, and base index methods for multiple trait selection in alfalfa for improvement of resistance to four alfalfa pests and recovery after cutting. Both index methods were the most effective, followed by modified independent culling levels and tandem selection, respectively.

MATERIAL AND METHODS

Cooperative research was initiated in 1980 between R. V. Frakes at Oregon State University and I. T. Carlson at Iowa State University on breeding for improved seed and forage characteristics in orchardgrass. Clones, polycross (PC) progenies, synthetics, and populations selected in Iowa for winterhardiness, disease resistance, and drought tolerance were established in replicated seed yield tests near Corvallis, Oregon. Ninety-eight clones were included in a clonal seed yield test; and 27 PC progenies, nine synthetics and populations, and several check varieties were included in a progeny seed yield test. The material in the clonal and progeny seed yield tests was also included in seed and forage yield tests planted near Ames, Iowa.

Meteorological and Geographical Data

Ames, Iowa, and Corvallis, Oregon, are situated approximately 3,218 km apart. A comparison of meteorological and geographical data for Ames and Corvallis follows:

	Ames	Corvallis
Degrees N. latitude	42:20	44:35
Degrees W. longitude	93:90	123:18
Plot elevation (m above sea level)	335	65
Precipitation (annual mean cm)	80.9	100.8
Daylength (hours-June 21)	15:15	15:30
Growing season (avg. days)	157	271

Orchardgrass seed production in the Willamette Valley is favored by a mild climate with a predominantly winter rainfall pattern and a growing season of 271 days. The harvesting season in July and August

is relatively dry with low relative humidity (Table 1). Winter is characterized by mild temperatures, very favorable for forage grass species with low winterhardiness such as orchardgrass.

Description of Materials

This research focuses on the performance of 28 clones and their polycross progenies derived from a medium to early maturing germplasm pool by selection for rust resistance, drought tolerance, spring vigor, and seed production. Also included were two populations and a synthetic derived from the germplasm pool, clones and synthetics derived from the cultivar "Sterling," and two Russian plant introductions (PIs). The following is a complete list and description of these materials. Syn-1 and Syn-2 refer to first and second generations, respectively.

A. Materials derived from medium to early maturing germplasm pool (EMGP):

1. Syn-1 of EMGP: derived from 32 clones selected for winterhardiness and rust resistance.

2. Syn-1 of 75-OGP: a composite of seed from about 550 plants selected for moderate to high rust resistance from Syn-1 of EMGP.

3. Syn-1 of 75-OGP-DR: a composite of seed from about 45 plants selected for rust resistance and for a low incidence of leaf disease at the time of seed harvest from the Syn-1 of EMGP.

4. Syn-2 of 76-OGP-DT: parents selected from the Syn-1 of EMGP for good vigor during dry weather of late summer 1976 and for rust resistance.

Table 1. Willamette Valley meteorological data: Corvallis, Oregon Station[a]

Month	Temperature (°C)[b]	Average precipitation (cm)[b]	Relative humidity (%)[c]
January	3.8	17.93	78
February	6.2	11.76	67
March	7.5	10.67	57
April	10.0	5.21	49
May	13.1	4.50	43
June	16.1	2.92	39
July	18.8	0.84	31
August	18.8	1.40	31
September	16.6	3.33	48
October	11.8	9.60	55
November	7.4	15.34	81
December	5.0	17.35	85
Year	11.26	100.85	55

[a]Taken from Youngberg (1980).

[b]30-year normal.

[c]11-year mean.

5. Twenty-eight parent clones and their polycross (PC) progenies: the clones were selected from the 52 parents of 76-OGP-DT for good spring vigor and seed production in a crossing block.

B. Material derived from Sterling by selection mainly for rust resistance, with some selection for winterhardiness and resistance to other diseases (C=cycle of selection, P and G=phenotypic and genotypic selection, respectively; and R=reconstituted):

1. Syn-2 and 3 of Sterling and its five parent clones.
2. Syn-2 of C1-PG and its six parent clones.
3. Syn-2 of C2-PR and 21 of 23 of its parent clones.
4. Syn-2 of C3-PG and its 10 parent clones.

C. Material derived from two late-maturing Russian PIs by selection for disease resistance (mainly rust) and winterhardiness:

1. Syn-1 of a synthetic from PI262459 (designated Syn 262459) and its 14 parent clones.
2. Syn-1 of a synthetic from PI315425 (designated Syn B315425) and 9 of 10 of its parent clones.
3. Six additional very late-maturing parent clones from PI315425.

Fifteen of the 32 parents of EMGP trace back to three two-clone crosses among clones of local origin. Two of the remaining 17 were selected from a Romanian PI, and the other 15 were selected from eight Russian PIs. Five of the 28 clones selected from the 52 parents of 76-OGP-DT trace back maternally to the two-clone crosses of local origin and the remaining 23 trace back to the eight PIs from Russia.

The material derived from Sterling was developed by recurrent selection as described by Miller and Carlson (1982). The parents of the final cycle, C3-PG, were selected from 39 third-cycle selections on the basis of topcross progeny performance.

Clonal Seed Yield Tests

These tests were designed to evaluate the parent clones of PC progenies and synthetics for seed production and related traits when grown near Corvallis, Oregon, and Ames, Iowa.

Oregon clonal seed yield test

The following entries were included in a clonal seed yield (CSY) test: the 28 parent clones of PC progenies derived from 76-OGP-DT; and the parent clones of Sterling, C1-PG, C3-PG, and Syn 262459. Also included were 20 of the 23 parent clones of C2-PR, 9 of the 10 parents of Syn B315425, and the six additional clones from PI315425, making a total of 98 entries.

The test was established on 29 April 1980 at the Hyslop Crop Science Field Laboratory near Corvallis, Oregon. A randomized complete-block design with five replications was used. Each plot consisted of a single propagule spaced 91 cm within and between rows. A single border row containing propagules of entries included in the test completely surrounded the experiment.

The test received broadcast applications of nitrogen fertilizer at the rate of 84 kg/ha in the fall of 1980 and 1981. In addition, the herbicide Karmex was applied at a rate of 3.4 kg/ha each fall. Irrigation water was applied in the spring of 1982 because of dry weather, otherwise the plots were dependent upon natural rainfall for moisture.

No seed yield determinations were made in 1980, the year of establishment. Seed yield and related traits were determined during the summers of 1981 and 1982.

Iowa clonal seed yield test

The entries included in the Oregon CSY test were also included in the Iowa CSY test. One additional parent clone of C2-PR (415-7)

was included in the Iowa test, making a total of 99 entries. The vigor of clone 415-7 was not sufficient for including it in the Oregon CSY test.

The test was established on 21 April 1981 at the Agronomy and Agricultural Engineering Research Center near Ames, Iowa. A randomized complete-block design with five replications was used. Each plot consisted of a single propagule spaced 61 cm within and between rows. A single border row containing propagules of entries included in the test completely surrounded the experiment.

The area was topdressed in the fall of 1980 with 112 kg/ha each of P_2O_5 and K_2O. No fertilizer was applied during the establishment year, 1981. During the spring of 1982 and 1983, the test was topdressed with 66 and 73 kg/ha of nitrogen, respectively. The plots at Ames were dependent upon natural rainfall for moisture.

No seed yield determinations were made in 1981, the year of establishment. Seed yield and related traits were determined during the summers of 1982 and 1983.

Progeny Seed Yield Tests

These tests were designed to evaluate the PC progenies, synthetics, and populations for seed production and related characters when grown near Corvallis, Oregon, and Ames, Iowa.

Oregon progeny seed yield test

The following entries were included in a progeny seed yield (PSY) test: 27 of the 28 PC progenies derived from 76-OGP-DT; the Syn-1

generation of EMGP, 75-OGP, 75-OGP-DR, Syn 262459, and Syn B315425; the Syn-2 generation of C1-PG, C2-PR, C3-PG, and 76-OGP-DT; the Syn-2 and 3 generations of the cultivar Sterling; the cultivars Latar, Hallmark, and Potomac; and the experimentals Oregon Late and Later. The PC progeny of clone 39-28 was not included in the test because of insufficient seed. Latar was derived from a Russian PI at Washington State University. It was selected for late-maturity, vigor, seed production, and high digestibility. Hallmark is comprised of five clones that were selected on the basis of vigor, recovery after cutting, leaf disease resistance, and seed yield in Oregon. Potomac was developed by the USDA at Beltsville, Maryland, and was selected for rust resistance, leafiness, persistence, and vigor. Oregon Late and Later are experimental synthetics developed at Oregon State University. Like Latar, they were selected for late-maturity, vigor, and seed production.

The PSY test was planted on 6 May 1980 at the Hyslop Crop Science Field Laboratory near Corvallis, Oregon. A randomized complete-block design with six replications was used. Each plot consisted of a single row 3.7 meters long and spaced 91 cm. The entries were seeded with Planet Jr seeders at a rate of approximately 11 kg/ha. The test was surrounded by a single border row with two border rows between ranges.

The test received broadcast applications of nitrogen fertilizer at the rate of 84 kg/ha in the fall of 1980 and 1981. In addition, the herbicide Karmex was applied at a rate of 3.4 kg/ha each fall. The plots were dependent upon natural rainfall for moisture.

No seed yield determinations were made in 1980, the year of establishment. Seed yield and related characters were determined during the summers of 1981 and 1982.

Iowa progeny seed yield test

The following entries were included in a PSY test: the 28 PC progenies derived from 76-OGP-DT; the Syn-1 generation of EMGP, 75-OGP, 75-OGP-DR, Syn 262459, and Syn B315425; the Syn-2 generation of 76-OGP-DT, Sterling, C1-PG, C2-PR, and C3-PG; and the cultivars Napier and Orion. Napier is comprised of eight clones that were selected on the basis of rust and leaf blight resistance, winterhardiness, and forage yield. Orion is a synthetic variety developed by Northrup King for late-maturity and high forage quality.

The PSY test was established on 17 April 1980 at the Agronomy and Agricultural Engineering Research Center near Ames, Iowa. A randomized complete-block design with four replications was used. Each plot consisted of a single row 3.7 meters long and spaced 91 cm. The entries were seeded with Planet Jr seeders at a rate of approximately 11 kg/ha. A single border row was planted on each side of the test.

The area was topdressed in the fall of 1979 with 112 kg/ha each of P_2O_5 and K_2O. No fertilizer was applied in 1980, the establishment year. In the spring of 1981, 1982, and 1983, a topdressing of 64, 101, and 91 kg/ha, respectively, of N was applied to the test. The plots were dependent upon natural rainfall for moisture.

No seed yield determinations were made in 1980, the year of establishment, and in 1981 because of dry weather. Seed yield and related traits were determined during the summers of 1982 and 1983.

Characters Studied

The following characters were evaluated in the CSY and PSY tests:

Anthesis date:

CSY tests: the number of days past April 30 when three panicles on a plant were shedding pollen.

PSY tests: the number of days past April 30 when approximately 50% of the panicles in a plot were shedding pollen.

Panicle number:

CSY tests: the number of panicles on a plant.

PSY tests: the number of panicles in a 0.914 meter sample of of row.

Girth (measured on CSY tests only):

The circumference (cm) below panicles when all the culms on a plant were grouped together.

Seed yield:

CSY tests: grams of clean seed determined from individual plants.

PSY tests: kg/ha of clean seed determined from 3.66 and 3.05 meters of row, respectively, at Corvallis and Ames.

Five panicles were randomly sampled from each plant in the CSY tests and 10 from each plot in the PSY tests for determination of the following characters:

Panicle length: the length (cm) from basal branch of panicle to tip of panicle.

Seed yield per panicle: the weight (mg) of clean seed from each sample of panicles divided by the number of panicles.

Fertility index: the weight of clean seed divided by the weight of unthreshed panicles for each sample and expressed as g/kg.

100-seed weight: the weight (mg) of 100 random seeds from each sample.

Seed number per panicle: was calculated by dividing the seed yield per panicle by the individual weight per seed.

All characters were determined at Corvallis in 1981 and 1982 and at Ames in 1982. In 1983, only anthesis date and seed yield were determined in the Iowa PSY test, while anthesis date, seed yield per panicle, fertility index, 100-seed weight, and seed yield were determined in the Iowa CSY test.

Progeny Forage Yield Test

To determine forage characteristics, the following entries were included in a progeny forage yield (PFY) test: the 28 PC progenies derived from 76-OGP-DT; the Syn-1 generation of 75-OGP; the Syn-2 generation of 76-OGP-DT, C2-PR, and C3-PG; the Syn-3 generation of Sterling; the cultivars Napier, Orion, Dart, Hawk, and Crown and the experimental synthetics DS-4 and NAPB 417901. Dart is a seven-clone synthetic developed by Land O'Lakes and derived from Sterling, Napier, Potomac, and a male-sterile clone. Hawk and Crown were developed by North American Plant Breeders (NAPB). Crown is a synthetic selected for rust resistance, general vigor, leafiness, and forage yield, while Hawk is a three-way hybrid between a male-sterile two-clone cross

and Crown. The experimentals DS-4 and NAPB 417901 were developed by Land O'Lakes and NAPB, respectively. DS-4 is a six-clone synthetic with three clones from Able and one each from Napier, Jackson, and Sterling. NAPB 417901 is a 10-clone synthetic selected for vigor and rust resistance.

The PFY test was planted on 17 April 1980 at the Agronomy and Agricultural Engineering Research Center near Ames, Iowa. A randomized complete-block design with four replications was used. Each plot consisted of six rows 3.7 meters long and spaced 23 cm. The entries were seeded with Planet Jr seeders at a rate of approximately 22 kg/ha.

The area was topdressed in the fall of 1979 with 112 kg/ha each of P_2O_5 and K_2O. No fertilizer was applied in 1980, the establishment year. In the spring of 1981, the test was topdressed with 90.7, 87.4, and 87.4 kg/ha of nitrogen, P_2O_5, and K_2O, respectively, and with 88 kg/ha of N after the first and second harvests. In 1982, a topdressing of 89.6, 87.4, and 87.4 kg/ha of N, P_2O_5, and K_2O, respectively, was applied on 14 April and 94.6 kg/ha of N after the first and second harvests. The test was topdressed in the spring of 1983 with 86.2, 97.4, and 97.4 kg/ha of N, P_2O_5, and K_2O, respectively, followed by applications of 97.4 and 81.5 kg/ha of N after the first and second harvests, respectively.

No yield determinations were made in 1980, the year of establishment. Plots were harvested three times in 1981, 1982, and 1983. The number of days past April 30 when 50% of the panicles per plot were estimated to be out of the boot stage was recorded each year.

On 1 June 1981 and on 8 June 1982, plots were rated for their relative amount of panicle production, using a scale from 1=least to 5=most panicles per plot. Plots were rated for leaf diseases on 4 September 1981 and on 8 June 1982 with a rating scale from 1=least to 5=most diseased leaf area. In 1981, the disease was mostly leaf streak with some rust. In 1982, the disease was mainly Rhyncosporium scald with some leaf streak. Rust ratings were taken on 22 September 1982 with a rating scale from 1=most resistance to 5=most susceptible. In vitro dry matter digestibility (IVDMD) was determined on duplicate samples of the forage from each plot in two replications at all harvests in both 1981 and 1982 by the two-state rumen fermentation technique adapted from the procedure of Tilley and Terry (1963).

Statistical Analyses

No analyses will be presented for the parent clones of Sterling, C1-PG, C2-PR, C3-PG, Syn 262459, and Syn B315425 because of a large number of missing plots. The Sterling-derived material was generally very poor in vigor possibly due to a root disease caused by Pythium sp., while missing plots in the material derived from the late-maturing Russian PIs were caused by the hot dry weather in spring of 1982 in Oregon. Since the information is not pertinent to the objectives of this study, no data will be presented for the following entries included in the Oregon PSY test: the Syn-3 generation of Sterling, the experimentals Oregon Late and Later, and the cultivar Latar. Similarly, no data will be presented for the following entries included in the Iowa

PFY test: the cultivars Dart, Hawk, and Crown; and the experimentals DS-4 and NAPB 417901. For uniformity, the analyses presented will concentrate on 27 of the 28 parent clones and their PC progenies, since the PC progeny 39-28 was not included in the Oregon PSY test.

Clonal and progeny seed yield tests

Analyses of variance were computed on all data with separate analyses for the parent clones and their PC progenies. The data were analyzed for each trait within evaluation years and locations. Plot means were analyzed for traits with more than one determination per plot. The analyses of variance over years and locations were computed using entry means. Variances were converted to a plot mean basis by multiplying by the harmonic mean of the number of replications. Years and locations (pooled together and called environments) and entries were considered random. Entries (clones or PC progenies) were considered as random variables for the following reasons: (1) they were relatively unselected for the characters under consideration; and (2) they would be representative of other breeding populations at this stage of development. Tables 2 and 3 illustrate, respectively, the form used in analyses of variance of seed yield data combined over years within a location and combined over years and locations. Some modifications in the format were necessary for traits not measured in 1983 at Ames.

Variance components were estimated from linear functions of mean squares from the analyses of variance. The component of variance arising from differences among clones (σ_c^2) is an estimate of the total genetic

Table 2. Expected mean squares for analyses of variance of clonal and progeny seed yield data combined over years within a location[a]

Source of variation	df	Mean square expectations
Years (Y)	y-1	$\sigma^2+r\sigma^2_{YE}+re\sigma^2_Y$
Entries (E)	e-1	$\sigma^2+r\sigma^2_{YE}+ry\sigma^2_E$
E X Y	(e-1)(y-1)	$\sigma^2+r\sigma^2_{YE}$
Pooled residual	Y(r-1)(e-1)	σ^2

[a]Where r=harmonic mean of number of replications; e=number of entries; y=number of years; and σ^2=pooled error variance, with replications, entries, and years considered random. E=C and F for the parent and PC progeny analyses of variance, respectively.

variance. While the component of variance arising from differences among PC progenies (σ^2_F) is equal to the covariance among half-sib (HS) families, which represents one-quarter of the additive genetic variance, plus one-sixteenth of the digenic variance (Levings and Dudley, 1963). The standard error (SE) of an estimated variance component was computed as the square root of the variance of the estimated variance component by the method described by Anderson and Bancroft (1952) and Kempthorne (1957).

Broad-sense heritabilities were estimated on a plot (H^2_p) and entry mean (H^2_E) basis as follows:

Table 3. Expected mean squares for analyses of variance of clonal and progeny seed yield data combined over years and locations[a]

Source of variation	df	Mean square expectations
Environments (E)[b]	e-1	$\sigma^2+r\sigma^2_{GE}+rg\sigma^2_E$
Ore vs. Iowa	1	$\sigma^2+r\sigma^2_{LG}+rg\sigma^2_L$
Among Ore Years	1	$\sigma^2+r\sigma^2_{OG}+rg\sigma^2_O$
Among Iowa Years	1	$\sigma^2+r\sigma^2_{IG}+rg\sigma^2_I$
Genotypes (G)[c]	g-1	$\sigma^2+r\sigma^2_{GE}+re\sigma^2_G$
G X E	(e-1)(g-1)	$\sigma^2+r\sigma^2_{GE}$
Ore vs. Iowa x G	26	$\sigma^2+r\sigma^2_{LG}$
Ore Years x G	26	$\sigma^2+r\sigma^2_{OG}$
Iowa Years x G	26	$\sigma^2+r\sigma^2_{IG}$
Pooled residual	e(r-1)(g-1)	σ^2

[a]Where r=harmonic mean of number of replications; g=number of entries; e=number of environments; L=variance component associated with locations; O and I=variance component associated with years at Oregon and Iowa, respectively; and σ^2=pooled error variance, with environments, entries, and replications considered random. G=C and F for the parent clone and PC progeny analyses of variance, respectively.

[b]Years and locations are pooled and called environments.

[c]Entries are designated genotypes.

$$H_p^2 = \frac{\sigma_C^2}{\sigma_p^2} = \frac{\sigma_C^2}{\sigma^2+\sigma_{CE}^2+\sigma_C^2}$$

$$H_E^2 = \frac{\sigma_c^2}{\sigma_p^2} = \frac{\sigma_c^2}{\sigma^2/re+\sigma_{CE/e}^2+\sigma_C^2}$$

where,

σ_C^2 = variance component due to parents;

σ_{CE}^2 = variance component due to parent x year or parent x environment interaction;

σ^2 = variance component due to pooled residuals;

r = harmonic mean of the number of replications; and

e = number of years or number of environments.

Since the parents were clones, the heritabilities calculated using parent variance components are equal to a ratio of the total genetic variance (σ_C^2) to the phenotypic variance among parents on a plot (σ_p^2) or on an entry mean basis ($\sigma_{\bar{p}}^2$). Narrow-sense heritabilities (h^2) were estimated on a family mean basis as follows:

$$h^2 = \frac{\sigma_F^2}{\sigma_{\bar{PF}}^2} = \frac{\sigma_F^2}{\sigma^2/re+\sigma_{FE/e}^2+\sigma_F^2}$$

where,

σ_F^2 = variance component due to HS families;

σ_{FE}^2 = variance component due to HS family x year or HS family x environment interaction;

σ^2 = variance component due to pooled residuals;

r = harmonic mean of the number of replications; and

e = number of years or number of environments.

Since the genetic variance among HS families represents primarily the additive genetic variance contained in the phenotypic variance among HS family means ($\sigma^2_{\overline{PF}}$), the heritability calculated is an estimation of the narrow-sense heritability on a family mean basis. Narrow-sense heritabilities were also estimated by parent-offspring regression as follows:

$$h^2 = 2(b_{op}) = \frac{\sigma^2_A}{\sigma^2_{\overline{P}}}$$

where,

h^2 = narrow-sense heritability estimate;

b_{op} = regression coefficient of the offspring variable on the parent variable;

σ^2_A = additive genetic variance component; and

$\sigma^2_{\overline{P}}$ = phenotypic variance among parent means.

Phenotypic and genotypic correlations were calculated utilizing entry means for both CSY and PSY data. Multiple linear regression techniques were used to determine the relative linear relationships of five seed-yield related traits to Oregon PSY according to Draper and Smith (1966).

To predict grains from selection, the following matrix equation was solved (Lin, 1978):

$$\Delta = \frac{ib'G}{(b'Pb)^{\frac{1}{2}}}$$

where,

Δ = vector of predicted gains;

i = standardized selection differential;

b' = row vector of b values;

G = genotypic variance-covariance matrix; and

P = phenotypic variance-covariance matrix.

To predict the correlated response in Oregon PSY when selection was based on traits determined in Iowa, the same equation was used. The b value for Oregon PSY was set equal to zero, while the b value(s) of the trait(s) being selected in Iowa were set equal to one.

Progeny forage yield test

Analyses of variance were computed on the data collected from the forage yield test. Data combined over harvests or years were analyzed, according to Steel and Torrie (1980), as a split plot in time with harvests and years as subplots. The expected mean squares for analyses of data combined over harvests and over years are presented in Tables 4 and 5, respectively.

Variance components and their standard errors were estimated for the forage traits. Narrow-sense heritabilities were estimated on a phenotypic mean basis as follows:

$$h^2 = \frac{\sigma_F^2}{\sigma_{PF}^2} = \frac{\sigma_F^2}{\sigma^2/ry+\sigma_{FY/Y}^2+\sigma_F^2}$$

where,

σ_F^2 = variance component due to HS families;

σ_{PF}^2 = phenotypic variance among HS family means;

Table 4. Expected mean squares for analysis of variance of forage yield data combined over harvests within years[a]

Source of variation	df	Mean square expectations
Replications (R)	r-1	$\sigma^2+h\sigma^2_\gamma+re\sigma^2_R$
Entries (E)	e-1	$\sigma^2+h\sigma^2_\gamma+rh\sigma^2_E$
Error (a)	(r-1)(e-1)	$\sigma^2+h\sigma^2_\gamma$
Harvests (H)	h-1	$\sigma^2+r\sigma^2_{HE}+e\sigma^2_{HR}+re\theta^2_H$
H x R	(h-1)(r-1)	$\sigma^2+e\sigma^2_{HR}$
H x E	(h-1)(e-1)	$\sigma^2+r\sigma^2_{HE}$
Error (b)	(r-1)(h-1)(e-1)	σ^2

[a]Where r=number of replications; e=number of entries; h=number of harvests; σ^2, σ^2_γ=error variances, with harvests considered fixed.

σ^2_{FY} = variance component due to HS family x year interaction; and

r, y = number of replications and years, respectively.

Analyses of seed and forage yield data

Phenotypic and genotypic correlations were calculated in all combinations for Oregon PSY and selected Iowa forage traits. The Smith-Hazel (SH) selection index was employed for the simultaneous improvement of Oregon PSY, Iowa PFY, IVDMD, and rust resistance. The general procedures used to compute the SH index were as follows:

Table 5. Expected mean squares for analyses of variance of forage yield data combined over years[a]

Source of variation	df	Mean square expectations
Replications (R)	r-1	$\sigma^2+y\sigma^2_\gamma+ye\sigma^2_R$
Entries (E)	e-1	$\sigma^2+y\sigma^2_\gamma+ry\sigma^2_E$
Error (a)	(r-1)(e-1)	$\sigma^2+y\sigma^2_\gamma$
Years (Y)	y-1	$\sigma^2+r\sigma^2_{YE}+e\sigma^2_{YR}+re\theta^2_Y$
Y x R	(y-1)(r-1)	$\sigma^2+e\sigma^2_{YR}$
Y x E	(y-1)(e-1)	$\sigma^2+r\sigma^2_{YE}$
Error (b)	(r-1)(e-1)(y-1)	σ^2

[a]Where r=number of replications; e=number of entries; Y=number of years; σ^2, σ^2_γ=error variances, with years considered fixed. E=F for the PC progeny analysis of variance.

Let $I = b_1P_1 + \ldots + b_nP_n$ and

$H = a_1G_1 + \ldots + a_nG_n$

where,

I = index value for a given phenotype;

b_n = index weight for trait n;

P_n = phenotypic value for trait n;

H = genotypic score for a given genotype;

a_n = measure of relative importance of trait n; and

G_n = genotypic value of trait n.

Maximizing the correlation between H and I allows for selection of phenotypes that have the greatest worth. This amounts to choosing the index weights (b's) such that genotypes with the highest score are selected. The method for deriving the index weights (b's) was developed by H. F. Smith in 1936 and is as follows:

$$\underline{b} = P^{-1}G\underline{a}$$

where,

$\underline{b}$ = vector of b values corresponding to the traits included in the index;

P^{-1} = the inverse of the phenotypic variance-covariance matrix;

G = the genotypic variance-covariance matrix; and

$\underline{a}$ = vector of relative economic weights.

The four traits were considered equally important. Relative economic values were assigned as +1 for Oregon PSY, Iowa PFY, and IVDMD, and -1 for rust resistance. Since the traits evaluated were on scales of much different magnitude, b values were calculated in standard units. Predicted gains from selection were estimated by the matrix formula given by Lin (1978), which was described previously in the section on clonal and progeny seed yield tests.

RESULTS

The results are presented in three sections: the first is concerned with data from the clonal and progeny seed yield tests; the second deals with data from the progeny forage yield test; and the last section concerns selection for improved seed and forage characteristics.

Seed Yield Tests

Performance of Iowa breeding material

The mean performance of PC progenies, populations, and synthetics for traits determined in the Oregon PSY test is presented in Table 6. All of the progenies, populations, and synthetics selected in Iowa for improved forage characteristics yielded significantly less seed than Hallmark and Potomac. Eleven of the PC progenies, however, were similar in seed yield to Sterling, a cultivar satisfactory in Oregon seed production (Table A1). Of the 27 PC progenies, 10-27 ranked highest in seed yield with a 1981-1982 average of 722 kg/ha.

Hallmark yielded significantly more seed over years than any other entry. It also ranked highest in panicle production, seed yield per panicle, and fertility index. It ranked second only to Potomac in 100-seed weight, it had long panicles, and it was early in maturity.

Sterling ranked highest in seed yield among the 10 Iowa-derived cultivars, populations, and synthetics. Of the three synthetics derived from Sterling, C2-PR was highest and similar to Sterling in seed yield and C3-PG yielded significantly less seed than the other two. EMGP and the synthetic and two populations derived from it were similar in

Table 6. Performance of polycross progenies, populations, and synthetics in a seed yield test near Corvallis, Oregon, 1981-82

Material	Seed yield (kg/ha)	Panicle number[a]	Seed yield/ panicle (mg)	No. seeds/ panicle	Panicle length (cm)	Fertility index (g/kg)	100-seed weight (mg)	Anthesis date[b]	Plant height (cm)
EMGP	523	270	355	471	18.5	498	81.4	28.9	136
75-OGP	553	276	408	428	19.5	497	83.4	29.2	141
75-OGP-DR	483	229	400	414	18.2	503	82.1	30.0	144
76-OGP-DT	538	228	473	553	19.5	510	86.2	31.0	149
27 PC progenies									
Mean	553	241	425	504	19.1	518	81.4	31.7	144
Range	371-722	178-294	333-507	372-610	16.8-21.5	456-573	72.2-93.5	28.9-39.5	135-151
Sterling	658	328	371	419	18.3	526	87.6	29.5	134
C1-PG	547	286	313	373	17.6	505	85.3	30.0	128
C2-PR	629	310	367	441	18.3	511	93.8	29.2	130
C3-PG	404	274	333	398	16.0	492	92.4	30.2	126
Syn. 262459	397	206	510	712	17.5	528	86.4	41.7	148
Syn. B315425	138	108	254	360	15.2	380	82.8	49.2	124
Hallmark	942	331	531	584	19.9	640	99.6	29.2	141
Potomac	849	261	479	455	18.4	628	102.0	29.2	146
Experiment mean	558	248	417	488	18.8	520	84.6	32.1	142
L.S.D., 0.05	90	40	72	120	1.4	40	9.6	1.8	6
C.V. %	20.1	14.1	21.5	17.2	9.5	9.6	8.0	7.0	5.5

[a]The number of panicles in a 0.914 meter sample of row.

[b]The number of days past April 30.

seed yield to each other and to the mean of the 27 PC progenies. Syn B315425, the latest-maturing entry, yielded significantly less seed than any other entry and it ranked lowest in all traits related to seed yield except 100-seed weight. The second latest-maturing entry, Syn 262459, ranked low in seed yield, evidently because of poor panicle production. It ranked high in seed yield per panicle.

Table 7 presents the mean performance of PC progenies, populations, and synthetics for all traits determined in the Iowa PSY test. The 27 PC progenies averaged higher in 1982-83 seed yield than any other entry except 76-OGP-DT. Of the 27 PC progenies, 12-12 ranked highest in seed yield with a 1982-83 average of 466 kg/ha (Table A3). Eleven progenies yielded more seed than 76-OGP-DT, the highest yielding of the 12 populations, synthetics, and cultivars. This was not consistent with findings from the Oregon PSY test where Sterling ranked highest in 1981-82 seed yield among the 10 Iowa-derived varieties, populations, and synthetics. The material derived from EMGP was superior in seed yield, on the average, to the Sterling- and Russian-derived material. As was found in the Oregon PSY test, EMGP and the synthetic and two populations derived from it were similar in 1982-83 seed yield to each other and to the mean of the 27 PC progenies.

Sterling, a cultivar selected for high seed yield in Iowa, was highest in both seed yield per panicle and fertility index in 1982 among the 10 Iowa-derived cultivars, populations, and synthetics. However, it was third lowest in 1982 seed yield. Iowa C2-PR ranked second, first, second, and third in 1982 seed yield, panicle production, seed

Table 7. Performance of polycross progenies, populations, and synthetics in a seed yield test near Ames, Iowa, 1982-83

Material	Seed yield (kg/ha) 1982	1983	1982-83	Panicle number[a]	Seed yield/ panicle (mg)
EMGP	335	347	341	257	281
75-OGP	365	339	352	267	356
75-OGP-DR	341	347	344	244	335
76-OGP-DT	398	349	374	282	317
27 PC progenies					
Mean	411	320	366	255	365
Range	286-580	198-417	308-466	197-320	251-505
Sterling	287	210	248	252	390
C1-PG	369	238	304	238	364
C2-PR	387	232	310	286	382
C3-PG	354	313	334	284	307
Syn. 262459	281	239	260	234	275
Syn. B315425	252	217	234	118	349
Napier	467	259	363	280	369
Orion	309	285	297	152	426
Experiment mean	393	309	351	250	360
L.S.D., 0.05	126	52	59	49	100
C.V. %	23.0	12.0	19.8	13.9	20.0

[a]The number of panicles in a 0.914 meter sample of row.

[b]Rated from 1=little to 5=severe lodging.

[c]The number of days past April 30.

1982						
No. seeds/ panicle	Panicle length (cm)	Fertility index (g/kg)	100-seed weight (mg)	Plant height (cm)	Lodging score[b]	1982-83 Anthesis date[c]
335	14.1	504	96.0	113	2.1	41.1
279	14.6	562	105.5	106	2.9	41.4
288	14.3	568	95.6	110	3.0	42.5
326	14.7	557	109.8	108	1.8	41.2
357	15.8	565	100.9	111	2.1	41.7
270-460	13.6-18.0	446-646	83.4-112.2	99-120	1.0-4.2	38.6-44.6
393	12.9	675	108.7	100	4.4	39.9
341	12.7	665	111.4	98	2.5	39.0
323	12.8	662	104.7	99	3.6	39.0
256	11.5	603	108.5	96	2.9	40.2
353	16.3	493	89.2	110	1.9	48.6
399	17.9	494	89.8	112	1.8	52.0
336	12.9	658	119.3	105	3.2	40.2
395	17.3	544	94.0	110	1.9	49.0
350	15.4	570	101.7	109	2.3	42.0
ns	1.4	70	16.6	6	0.9	1.0
19.0	6.5	8.7	8.1	3.9	29.0	2.5

yield per panicle, and fertility index, respectively. Syn B315425 and 262459, the latest-maturing entries, ranked low in 1982 seed yield and panicle production. This was consistent with findings in the Oregon PSY test.

Variability among parent clones and their polycross progenies

Analyses of variance of the clonal and PC progeny seed yield data combined over years and locations are presented in Tables 8-11. Significant differences ($P \leq 0.01$) were found among environments (year-location combinations) for all traits. Location and year means are presented in Table 12. Location comparisons were unequal for different traits because some traits were evaluated for two years and some for one year in Iowa, whereas all traits were evaluated for two years in Oregon. Oregon seed yield was significantly ($P \leq 0.01$) greater than Iowa seed yield for both clones and progenies. Two-year average seed yields in Oregon were 39 and 51% greater than in Iowa for clones and progenies, respectively.

Identification of the components contributing to the greater seed yield in Oregon cannot be done completely because of only one year's data for some traits at Ames; however, greater seed yield per panicle in Oregon seemed to be a factor (Table 12). More seeds per panicle rather than higher weight per seed seemed to be the main factor in greater seed yield per panicle in Oregon. In fact, 100-seed weight was significantly higher for progenies in Iowa and it averaged higher in Iowa for the clones, also. For the progenies, larger panicles, as reflected by panicle length, seemed to be more important than seed set

Table 8. Analyses of variance of data combined over four environments from the clonal seed yield tests

Source of variation	df	Mean squares				
		Seed yield	Seed yield/ panicle	Fertility index	100-seed weight	Anthesis date
Environments (E)	3	24485.65**	4422184.90**	536139.89**	712.29*	3699.31**
Oregon vs. Iowa	1	14624.85*	8480171.70**	389996.52**	771.42	9081.50**
Among Iowa years	1	16532.05**	2091709.60**	849784.65**	1076.68**	1665.08**
Among Oregon years	1	42300.08**	2694673.40**	368639.27**	288.78	351.35**
Genotypes (G)	26[a]	2918.65**	233981.55**	77850.63**	1638.14**	426.34**
G x E	78	1359.15**	72174.83**	16561.49**	182.19**	31.40**
G x Oregon vs. Iowa	26	2208.77**	77794.70**	14890.95**	242.72**	59.86**
G x Iowa years	26	461.79*	41270.96	26446.71**	32.09	4.32
G x Oregon years	26	1406.92**	97458.90**	8346.73**	271.77**	30.02**
Pooled residual	416[b]	268.20	31719.70	4105.83	111.52	7.35

[a]Only 25 parents were used for fertility index.

[b]Residual degrees of freedom were 404, 354, 352, 102, and 406, respectively, for seed yield, seed yield per panicle, fertility index, 100-seed weight, and anthesis date.

*,**Significant at the 5 and 1% levels, respectively.

Table 9. Analyses of variance of data combined over three environments from the clonal seed yield tests

Source of variation	df	Mean squares				
		Panicle number	No. seeds/ panicle	Panicle length	Plant height	Girth
Environments (E)	2	182988.70**	1682097.40**	338.48**	51544.50**	913.21**
Oregon vs. Iowa	1	215078.50**	1918671.20**	152.92*	64088.90**	35.89
Among Oregon years	1	150898.85**	1445523.20**	524.03**	39000.00**	1790.53**
Genotypes (G)	26	9821.25**	129051.68**	95.11**	1247.64**	57.20**
G x E	52	5409.25**	60772.66*	27.25**	434.06**	24.30**
G x Oregon vs. Iowa	26	6454.50**	34485.60	29.20**	680.31**	25.36**
G x Oregon years	26	4364.05**	87059.70**	25.29**	187.79**	23.24**
Pooled residual	305[a]	1366.06	36673.10	7.78	121.38	9.12

[a]Residual degrees of freedom were 306, 76, and 304, respectively, for panicle number, number of seeds per panicle, and plant height.

*,**Significant at the 5 and 1% levels, respectively.

Table 10. Analyses of variance of data combined over environments from the progeny seed yield tests

Source of variation	df	Mean squares				
		Seed yield	Anthesis date	Panicle number	Seed yield/ panicle	No. seeds/ panicle
Environments (E)	3[a]	5439227.90**	5241.00**	32422.28**	4862183.00**	2291478.80**
Oregon vs. Iowa	1	4564007.60**	12799.68**	13753.40	334459.80**	777664.20**
Among Iowa years	1	11214092.00**	1178.62**	--	--	--
Among Oregon years	1	539583.76**	1744.71**	51091.12**	9389906.20**	3805293.20**
Genotypes (G)	26	62116.40**	65.41**	4406.52	21125.40	14354.94
G x E	78[b]	20467.59**	7.11**	3887.88**	12909.68**	8906.20
G x Oregon vs. Iowa	26	30213.87**	10.97**	6238.44**	14268.38**	6874.20
G x Iowa years	26	13488.58**	3.23	--	--	--
G x Oregon years	26	17700.30**	7.12**	1537.28**	11550.98**	10938.18
Pooled residual	416[c]	7369.39	3.40	973.40	6733.40	8121.38

[a]Environment degrees of freedom were 2 for panicle number, seed yield/panicle, and number of seeds/panicle.

[b]G x E degrees of freedom were 52 for panicle number, seed yield/panicle, and number of seeds/panicle.

[c]Residual degrees of freedom were 260, 338, and 77, respectively, for panicle number, seed yield/panicle, and number of seeds/panicle.

*,**Significant at the 5 and 1% levels, respectively.

Table 11. Analyses of variance of data combined over environments from the progeny seed yield tests

Source of varition	df	Mean squares			
		Panicle length	Fertility index	100-seed weight	Plant height
Environments (E)	2	1157.32**	1563737.10**	8808.90**	74101.07**
Oregon vs. Iowa	1	1023.80**	208103.18**	13778.84**	10253.75**
Among Oregon years	1	1290.84**	2919370.90**	3838.96**	45668.39**
Genotypes (G)	26	18.78**	11981.34	264.44**	291.38**
G x E	52	4.44**	10228.60**	91.24**	74.39**
G x Oregon vs. Iowa	26	5.14**	13184.10**	53.44	72.84**
G x Oregon years	26	3.74	7273.10**	129.06**	75.92**
Pooled residual	338[a]	2.46	2462.06	36.96	40.48

[a]Residual degrees of freedom for 100-seed weight were 77.

*,**Significant at the 5 and 1% levels, respectively.

as determined by fertility index, in the higher number of seeds per panicle in Oregon. On the average, the clones and progenies shed pollen eight and ten days earlier, respectively, in Oregon than Iowa. The clones grew taller in Iowa in 1982 than in Oregon, whereas the opposite was true for the progenies.

Significant differences ($P \leq 0.01$) were found between years for all traits in Oregon except 100-seed weight of the clones (Tables 8-11). Seed yield was much higher in 1982 for both the clones and progenies (Table 12). Higher seed yield in the second year could be attributed to both more panicles per plant and higher seed yield per panicle for the clones and to just the latter trait for the progenies. Both higher

Table 12. Year and location means for seed yield and other traits determined on parents and PC progenies

Trait	Parents						Progenies					
	Corvallis			Ames			Corvallis			Ames		
	1981	1982	81-82	1982	1983	82-83	1981	1982	81-82	1982	1983	82-83
Seed yield[a]	24.6	49.6	37.1	34.5	18.9	26.7	345	761	553	411	320	366
Panicle number[b]	53	100	77	126	--	--	256	226	241	255	--	--
Seed yield/panicle (mg)	524	740	632	456	266	361	241	609	425	365	--	--
No. seeds/panicle	608	839	723	493	--	--	316	692	504	357	--	--
Panicle length (cm)	15.8	18.6	17.2	18.5	--	--	16.9	21.2	19.1	15.8	--	--
Fertility index[c] (g/kg)	533	616	574	577	451	514	415	620	518	565	--	--
100-seed weight (mg)	87.8	91.1	89.4	96.4	90.2	93.2	75.4	87.3	81.4	100.9	--	--
Anthesis date[d]	34.6	32.3	33.5	39.2	44.2	41.7	29.1	34.3	31.7	39.5	43.8	41.7
Plant height (cm)	118	94	106	132	--	--	157	131	144	111	--	--

[a]Seed yield was determined in g/plant and kg/ha for parents and progenies, respectively.

[b]The number of panicles per plant and per 0.914 meter of row for parents and progenies, respectively.

[c]Values based on 25 parents and PC progenies.

[d]The number of days past April 30.

100-seed weight and a greater number of seeds per panicle seemed to be factors in the higher 1982 seed yield per panicle for the progenies, whereas only number of seeds per panicle seemed to be an important factor for the clones. Both larger panicles and higher seed set seemed to contribute to the much higher number of seeds per panicle in 1982 for both clones and progenies.

In Iowa, seed yield decreased from 1982 to 1983 for both clones and progenies. Traits contributing to this decrease cannot be determined completely because of incomplete data; however, seed yield per panicle, fertility index, and 100-seed weight all decreased from 1982 to 1983 for the clones. Anthesis occurred later in 1983 than in 1982 for both clones and progenies.

There were significant differences among clones and among their PC progenies in mean performance over environments (location-year combinations) for all traits except panicle number, seed yield per panicle, seed number per panicle, and fertility index of the progenies (Tables 8-11). Genotypes interacted significantly with year-location combinations for all traits except seed number per panicle for the progenies. The genotype by location interactions were significant for all traits except for seed number per panicle for both clones and progenies and for 100-seed weight of the progenies. Genotypes interacted significantly with years within locations for all traits except number of seeds per panicle and panicle length of progenies in Oregon; seed yield per panicle, 100-seed weight, and anthesis date of clones in Iowa; and anthesis date of progenies in Iowa. Individual clonal and progeny means in each environment are presented in Tables A1-A7.

Estimates of genotype, genotype by environment, and error variance components are reported in Table 13. The genotype by location component was more than twice as large as the genotype component for seed yield and panicle number of both clones and progenies; for seed yield per panicle and fertility index of the progenies; and for plant height of the clones. These two components were similar in magnitude for seed yield per panicle and panicle length of the clones. The genotype component was much larger than the genotype by location component for panicle length and plant height of the progenies; 100-seed weight and anthesis date of both clones and progenies; and fertility index of the clones.

The correlation coefficients between locations reflect the relative size of these two components (Table 14). Thus, the r-values are nonsignificant or relatively low for seed yield and panicle number of both clones and progenies; for seed yield per panicle, seed number per panicle, and fertility index of the progenies; and for plant height of the clones. The r-values range from 0.71 to 0.92 for 100-seed weight and anthesis date of both clones and progenies, and for fertility index of the parents.

The component of variance due to interaction of genotypes by locations usually was larger than components due to interaction of genotypes by years within locations (Table 13). Exceptions were genotypes by years in Oregon for seed yield per panicle and number of seeds per panicle of clones and for 100-seed weight of both clones and progenies, and genotypes by years in Iowa for fertility index of clones.

Table 13. Estimates of variance components and their standard errors for seed yield and other characters of parents and PC progenies when analyzed over environments

Trait	Genotype	σ^2_G	Genotype x environment			σ^2
			G x Ore. vs. Ia	G x Ore. years	G x Ia years	
Seed yield[a]	Parent	78.0±40.5**	388.1±118.1**	227.7±75.3**	38.7±25.0*	268.2±18.6
	Progeny	2169±881**	4759±1686**	2152±991**	1275±759**	7369±511
Panicle number[b]	Parent	294.1±188.3*	1018±346**	600±123**	--	1366.1±110.1
	Progeny	43.2±116.3	1175±417**	141±105**	--	973.4±85.1
Seed yield/panicle	Parent	9429±3704**	10751±2923**	15339±6103**	2229±2633	31720±2377
	Progeny	533±399	1465±748**	110±81**	--	6733±516
No. seeds/panicle	Parent	11380±6070**	0	25193±11999**	--	36673±5872
	Progeny	888±695	0	1408±1598	--	8121±1292
Panicle length	Parent	4.5±1.7**	4.3±1.6**	3.5±1.4**	--	7.8±0.6
	Progeny	0.9±0.3**	0.5±0.3**	0.2±0.2	--	2.5±0.2
Fertility index	Parent	3571±1268**	2514±965**	988±544**	5208±1711**	4205±309
	Progeny	114±244	2085±686**	935±380**	--	2462±189
100-seed weight	Parent	182.0±54.8**	65.6±33.3**	80.1±37.1**	0	111.5±15.5
	Progeny	28.9±12.1**	8.2±7.7	46.1±17.5**	--	37.0±5.9

[a]Seed yield was determined in g/plant and kg/ha for parents and progenies, respectively.

[b]Panicle number was determined as the number of panicles per plant and per 0.914 meter of row for parents and progenies, respectively.

*,**Mean square associated with variance component was significant at the 5 and 1% level, respectively.

Table 13. Continued

Trait	Genotype	σ^2_G	Genotype x environment			σ^2
			G x Ore. vs. Ia	G x Ore. years	G x Ia years	
Anthesis date	Parent	19.8±5.7**	10.5±3.2**	4.5±1.6**	0	7.4±0.5
	Progeny	3.1±0.9**	1.6±0.6**	0.8±0.4**	0	3.4±0.2
Plant height	Parent	55.2±22.9**	111.8±36.4**	13.3±10.2**	--	121.0±9.8
	Progeny	14.1±5.1**	6.1±3.7**	6.6±3.9**	--	41.0±3.1

Table 14. Phenotypic correlations between locations and between years within locations for traits determined in seed yield experiments

Trait	Between locations		Between years			
			Iowa		Oregon	
	Clonal test	Progeny test	Clonal test	Progeny test	Clonal test	Progeny test
Seed yield	0.19	0.38*	0.29	0.32	0.83**	0.63**
Panicle number	0.07	-0.28	--	--	0.83*	0.63**
Seed yield/panicle	0.57**	0.18	0.35	--	0.43*	0.26
No. seeds/panicle	0.51**	0.28	--	--	0.19	0.12
Panicle length	0.46**	0.52**	--	--	0.67**	0.62**
Fertility index	0.73**	0.09	0.28	--	0.68**	0.03
100-seed weight	0.78**	0.71**	0.95**	--	0.45*	0.09
Anthesis date	0.92**	0.81**	0.94**	0.87**	0.86**	0.79**
Plant height	0.15	0.60**	--	--	0.79**	0.47**

*,** Significant at the 5 and 1% levels, respectively.

Tables 15 and 16 summarize the variability expressed among clones and PC progenies within locations. Within states, differences among clonal means over years were significant for all traits except seed yield in Iowa and seed number per panicle in Oregon. Differences among progenies were significant for all traits except seed yield per panicle in Oregon, seed number per panicle in both states, and fertility index and 100-seed weight in Oregon. Genotype by year interactions were significant for all traits except 100-seed weight and plant height of

Table 15. Ranges of means, genetic and error CV's, and estimates of broad-sense heritability for traits determined in clonal seed yield tests

Trait	Location	Range	Genetic CV	Error CV
Seed yield (g/plant)[a]	Iowa	11.8-42.0	22.0	19.8
	Oregon	8.6-76.2	46.0	58.2
Panicles/plant	Iowa	51-173	22.0	22.4
	Oregon	27-148	35.1	52.8
Seed yield/panicle (mg)[a]	Iowa	199-554	19.3	23.8
	Oregon	350-974	19.4	35.4
No. seeds/panicle	Iowa	268-791	23.7	22.4
	Oregon	409-1188	13.3	30.7
Panicle length (cm)	Iowa	14.1-23.2	11.8	8.4
	Oregon	9.8-24.7	15.7	18.9
Fertility index (g/kg)[a]	Iowa	371-640	9.6	8.5
	Oregon	410-702	11.4	13.6
100-seed weight (mg)[a]	Iowa	61.5-131.6	18.5	5.9
	Oregon	66.6-114.3	11.1	10.7
Anthesis date[b]	Iowa	36.7-48.6	7.5	2.7
	Oregon	26.7-48.1	17.7	11.0
Plant height (cm)	Iowa	113-144	11.8	4.9
	Oregon	84-128	11.0	12.0

[a]Traits measured for two years at Iowa.

[b]The number of days past April 30.

*,**Mean square associated with variance component was significant at the 5 and 1% levels, respectively.

σ^2_G	σ^2_{GY}	σ^2	H^2_P	H^2_E
36±25	78±25**	28±3	0.24±0.17	0.45±0.32
291±121**	188±76**	465±46	0.31±0.13	0.67±0.28
765±248**	--	798±110	0.49±0.16	0.83±0.27
729±333**	542±280**	1654±163	0.25±0.11	0.63±0.23
4852±2884**	7644±2581**	7408±225	0.24±0.14	0.50±0.30
15350±8000**	12700±6000**	50005±4951	0.19±0.10	0.57±0.30
13671±5521**	--	12146±3246	0.53±0.21	0.85±0.34
9247±10126	18816±12603**	49427±9693	0.12±0.13	0.30±0.33
4.7±1.4**	--	2.4±0.3	0.66±0.19	0.91±0.27
7.3±2.7**	3.0±1.4**	10.6±1.0	0.35±0.13	0.74±0.28
2444±1755**	5657±1710**	1901±219	0.24±0.18	0.44±0.32
4310±1490**	735±553*	6050±614	0.39±0.13	0.82±0.28
295.7±81.2**	0.7±5.2	30.6±5.9	0.90±0.27	0.97±0.27
98.5±48.1**	90.0±37.4**	91.8±18.0	0.35±0.17	0.59±0.17
9.9±2.8**	0.6±0.2**	1.3±0.1	0.84±0.23	0.96±0.27
35.3±10.3**	3.3±1.6**	13.6±1.3	0.68±0.20	0.92±0.17
71±21**	--	42±10	0.63±0.19	0.89±0.26
134±40**	6±10	162±20	0.44±0.13	0.87±0.26

Table 16. Ranges of means, genetic and error CV's, and estimates of narrow-sense heritability for traits determined in progeny seed yield tests

Trait	Location	Range	Genetic CV	Error CV
Seed yield (kg/ha)[a]	Iowa	308-466	10.0	17.1
	Oregon	371-722	12.1	20.1
Panicle number[b]	Iowa	197-320	10.2	14.1
	Oregon	178-294	10.5	12.0
Seed yield/panicle (mg)	Iowa	251-505	12.0	19.0
	Oregon	333-507	6.7	16.3
No. seeds/panicle	Iowa	270-460	10.2	19.6
	Oregon	372-610	5.1	19.6
Panicle length (cm)	Iowa	13.6-18.0	7.3	6.0
	Oregon	16.8-21.5	5.7	8.9
Fertility index (g/kg)	Iowa	446-646	9.3	7.6
	Oregon	456-573	1.2	9.6
100-seed weight (mg)	Iowa	83.4-112.2	7.6	6.7
	Oregon	72.2-93.5	3.0	7.0
Anthesis date[a,c]	Iowa	38.6-44.6	3.2	2.1
	Oregon	28.9-39.5	7.1	7.0
Plant height (cm)	Iowa	99-120	4.9	3.4
	Oregon	135-151	2.5	4.9

[a]Traits determined for two years at Iowa.

[b]The number of panicles in a 0.914 meter sample of row.

[c]The number of days past April 30.

*,**Mean square associated with variance component was significant at the 5 and 1% levels, respectively.

σ^2_G	σ^2_{GY}	σ^2	h^2	$2b_{op}$	r_{op}
1336±823*	1833±759**	3907±442	0.49±0.30	3.12	0.33
4542±1776**	1620±1002**	12405±1084	0.71±0.28	3.95	0.55**
676±271**	--	1287±203	0.68±0.27	0.62	0.30
640±229**	175±105**	839±87	0.77±0.27	0.63	0.37
1950±900**	--	4822±762	0.60±0.28	0.19	0.23
750±600	1000±600**	4800±400	0.47±0.35	0.30	0.57**
1331±1205	--	4902±1310	0.35±0.32	0.20	0.22
651±1163	588±1742	9762±1896	0.19±0.34	0.22	0.34
1.3±0.4**	--	0.9±0.1	0.85±0.27	0.82	0.76**
1.2±0.4**	0.2±0.2	2.9±0.3	0.76±0.27	0.62	0.79**
2776±914**	--	2493±394	0.82±0.27	0.77	0.62**
41±275	1007±380**	2448±214	0.05±0.37	0.06	0.09
59.3±22.9**	--	46.0±12.3	0.72±0.28	0.82	0.82**
6.0±13.4	48.4±17.5**	32.4±6.3	0.16±0.35	0.84	0.88**
1.8±0.6**	0.5±0.2**	0.8±0.1	0.84±0.27	0.90	0.83**
5.1±1.6**	0.7±0.4**	5.0±0.4	0.87±0.27	0.69	0.89**
26±8**	--	14±2	0.92±0.25	0.90	0.72**
13±6**	6±4**	49±4	0.24±0.12	0.22	0.33

the clones in Iowa and Oregon, respectively, and number of seeds per panicle and panicle length of the progenies in Oregon.

It is of interest to compare the relative magnitude of the genotype and genotype by year components of variance in Tables 15 and 16. For the Oregon tests, the genotype component was larger than the genotype by year component for seed yield, panicle number, panicle length, anthesis date, and plant height of both clones and progenies; and for seed yield per panicle and fertility index of the clones. The genotype by year component was larger than the genotype component for seed yield per panicle, fertility index, and 100-seed weight of the progenies; and for number of seeds per panicle of the clones.

The correlation coefficients between Oregon years reflect the relative size of these two components (Table 14). Hence, the r-values ranged from 0.62 to 0.86 for seed yield, panicle number, panicle length, and anthesis date of both clones and progenies, and for fertility index and plant height of the clones, whereas they were low and nonsignificant for seed yield per panicle, fertility index, and 100-seed weight of the progenies; and for seed number per panicle of both clones and progenies.

For the Iowa test, the genotype component was more than three times as large as the genotype by year component for 100-seed weight and anthesis date of the clones, and for just the latter trait of the progenies (Tables 15 and 16). The genotype by year component was larger than the genotype component for seed yield of both clones and progenies, and for seed yield per panicle and fertility index of the clones.

As was found for Oregon, the correlation coefficients between Iowa years agree well with the relative size of these two components. The correlation coefficients ranged from 0.87 to 0.95 for anthesis date of both clones and progenies, and for 100-seed weight of the clones. The r-values were low and nonsignificant for seed yield of both clones and progenies; and for seed yield per panicle and fertility index of the clones.

The genetic component of variance (σ^2_G) among progenies was considerably smaller than that among parents for the last seven traits in Tables 15 and 16, except fertility index in Iowa. This was expected since variation among half-sib progenies accounts for only one-quarter of the additive and one-sixteenth of the digenic genetic variance among parent clones. The range among entry means was also greater for parents than for the progenies for those traits. For seed yield and panicle number, it is not valid to compare genetic components of variance and ranges of parents and progenies because of differences in units of determination. Genetic CVs were larger for parents than progenies for all traits.

There was a greater range among clonal means in Oregon than in Iowa for all traits except 100-seed weight. For the progenies, the range among means was greater in Oregon than Iowa for seed yield, number of seeds per panicle, panicle length, and anthesis date.

Heritability estimates calculated from components of variance (H^2_p, H^2_E, and h^2) varied widely among traits, between states, and between clones and progenies (Tables 15 and 16). Consistently high estimates

ranging from 0.84 to 0.96 on an entry mean basis were obtained for anthesis date. Heritability values for seed yield were higher for Oregon than Iowa for both clones and progenies (0.67 and 0.71 in Oregon and 0.45 and 0.49 in Iowa for clones and progenies, respectively). Considering components of seed yield, estimates were higher for panicle number than for seed yield per panicle; and they were higher for 100-seed weight than for number of seeds per panicle, except for the progenies in Oregon, where low estimates were obtained for both traits. Heritability estimates were consistently high for panicle length ranging from 0.74 to 0.91 on an entry mean basis. High estimates were also obtained for plant height except for the progenies in Oregon.

Oregon and Iowa heritability estimates are not strictly comparable for traits evaluated in only one year in Iowa. Genotype by year interaction variance may have inflated the genetic component of variance estimated for those traits from Iowa data.

Heritabilities estimated from the regression of progenies on parents and from parent-progeny correlations indicate the effectiveness of selection on the basis of clonal performance. The parent-progeny correlation is a heritability estimate in standard units (Frey and Horner, 1957). It eliminates the effects of any environmental or non-environmental factors which tend to reduce or increase the phenotypic variation among parents or progenies. Within states, significant parent-progeny correlations were obtained for seed yield and seed yield per panicle in Oregon; panicle length, 100-seed weight, and anthesis date in both states; and fertility index and plant height in Iowa

(Table 16). The r-values were highest for panicle length, 100-seed weight and anthesis date, ranging from 0.76 to 0.89. Estimates obtained from the regression of progenies on parents agree fairly well with estimates obtained from parent-progeny correlation for all traits except seed yield and panicle number. A regression value ($2b_{op}$) greater than one resulted for seed yield because of the different units of determination for parents and progenies.

The parent-progeny regressions and correlations calculated from Iowa clones and Oregon progeny means are of particular interest because they indicate the effectiveness of clonal selection in Iowa in relation to progeny performance in Oregon (Table 17). Significant r-values were obtained for seed yield per panicle, panicle length, 100-seed weight, anthesis date, and plant height, with relatively high values of 0.73 and 0.88 for 100-seed weight and anthesis date, respectively. The values obtained by parent-offspring regression agree fairly well with parent-progeny correlations for all traits except seed yield and anthesis date. The value from parent-progeny regression was greater than 1.0 for anthesis date, while it was much larger than the parent-progeny correlation for seed yield. There was a fairly good relationship between parents and progenies for seed yield of 21 of 27 pairs; however, the relationship was poor for six pairs (Figure 1). Clone 10-27 ranked lowest in clonal seed yield in Iowa, while its progeny ranked highest in seed production in Oregon. Similar results were found for clones 16-09, 31-09, and 18-21. Clones 10-32 and 03-08 were above average in Iowa clonal seed yield, but their progenies were well

Table 17. Iowa parent-Oregon progeny regression and correlation coefficients for traits determined in seed yield tests

Trait	$2b_{op}$	r_{op}
Seed yield	0.60	0.04
Panicle number	0.01	0.01
Seed yield/panicle	0.46	0.53**
No. seeds/panicle	0.26	0.32
Panicle length	0.40	0.39**
Fertility index	0.16	0.24
100-seed weight	0.52	0.73**
Anthesis date	1.32	0.88**
Plant height	0.50	0.49**

**Significant at the 1% level.

below average in Oregon seed production. Clone 04-04 demonstrated well below average performance for both Iowa clonal and Oregon progeny seed yield.

Intercharacter correlations

Relationships between seed yield and other traits also must be considered in breeding for high seed production in forages. High seed yield in Oregon was associated with high seed yield per panicle, long panicles, and early maturity in both the clonal and progeny tests (Table 18). In addition, clonal seed yield was positively associated with panicle number, seed number per panicle, fertility index, plant

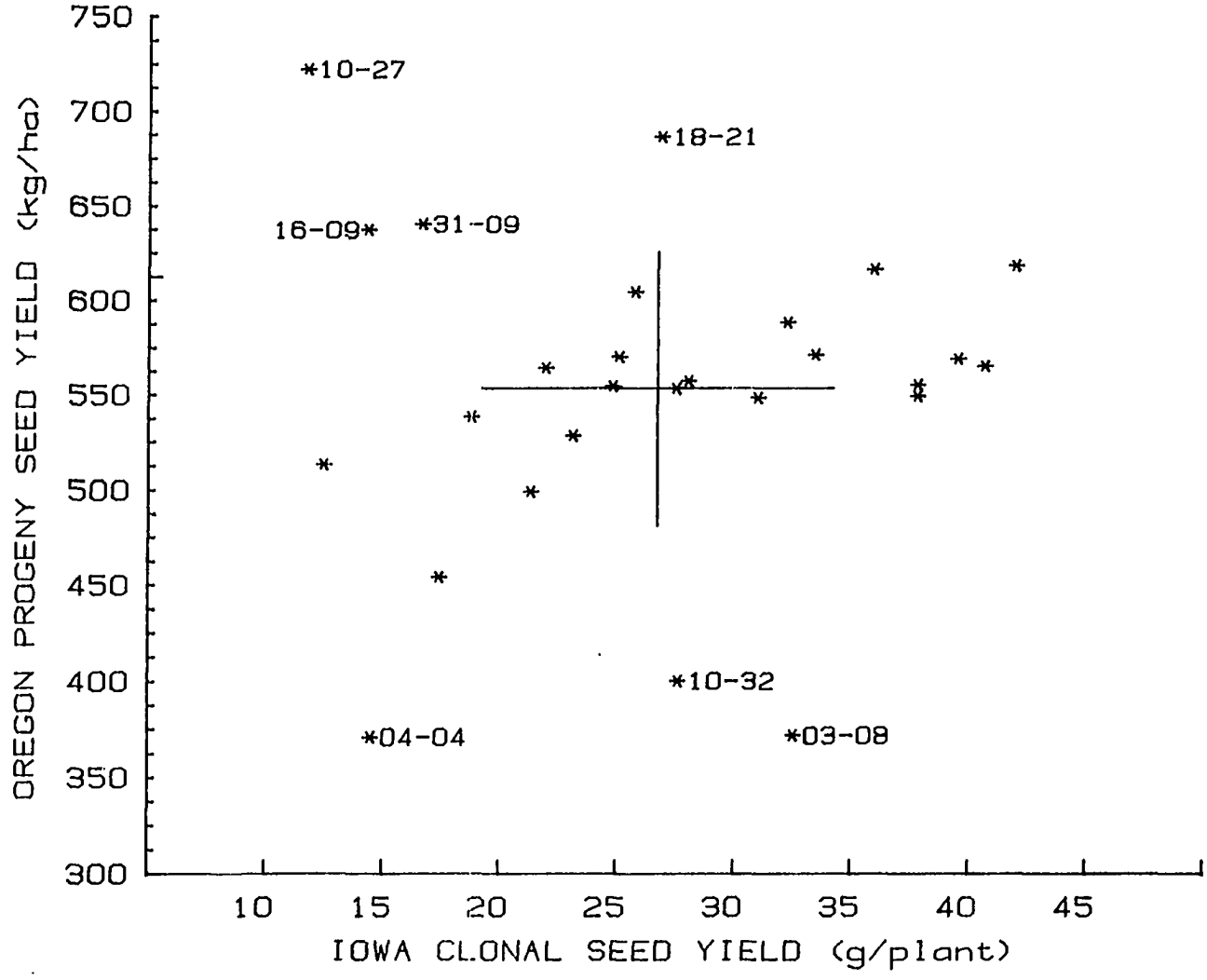

Figure 1. Scatter diagram of Oregon progeny seed yield with Iowa clonal seed yield

Table 18. Phenotypic correlations among traits determined in Oregon seed yield experiments, 1981-82[a]

Trait	Seed yield	Panicle number	Seed yield/ panicle	No. seeds/ panicle	Panicle length	Fert. index	100-seed weight	Anthesis date	Plant height	Girth
Seed yield		0.88**	0.61**	0.49**	0.69**	0.54**	0.30	-0.46*	0.87**	0.87**
Panicle number	0.30		0.32	0.29	0.49**	0.55**	0.14	-0.41*	0.81**	0.86**
Seed yield/panicle	0.43*	-0.47*		0.82**	0.68**	0.39**	0.44*	-0.44*	0.52**	0.49**
No. seeds/panicle	0.00	-0.62**	0.60**		0.54**	0.34	0.02	-0.29	0.46*	0.40*
Panicle length	0.71**	0.05	0.54**	0.20		0.18	0.30	-0.48**	0.55**	0.67**
Fertility index	0.36	-0.33	0.65**	0.48**	0.20		0.26	-0.77**	0.50**	0.29
100-seed weight	0.38*	-0.21	0.58**	0.01	0.37	0.29		-0.32	0.15	0.26
Anthesis date	-0.75**	-0.43*	-0.17	0.27	-0.47*	-0.06	-0.36		-0.35	-0.25
Plant height	-0.01	-0.30	0.05	0.16	0.17	-0.05	-0.23	0.16		0.81**
Girth	--	--	--	--	--	--	--	--	--	

[a]Parent clone and progeny correlations are above and below diagonal line, respectively.

*,**Significant at the 5 and 1% levels, respectively.

height, and girth. Girth was positively correlated with panicle number as expected (r=0.86) and its correlation with seed yield (r=0.87) was similar to the correlation between panicle number and seed yield (r=0.88). High seed yield per panicle was associated with high seed number per panicle, long panicles, high fertility index, and high 100-seed weight for both clones and progenies. Later-maturing plants in Oregon showed a tendency to produce shorter panicles than earlier-maturing plants. High r-values were obtained between panicle number and plant height and between fertility index and anthesis date (0.81 and -0.77, respectively) for the clones. High seed yield per panicle and high seed number per panicle tended to be associated with relatively few panicles for the progenies (r=-0.47 and -0.62, respectively). Intercharacter correlations for 1981 and 1982 in Oregon are presented in Tables A8 and A9.

Seed yield in Iowa was associated in a positive manner with panicle number, seed yield per panicle, and number of seeds per panicle for both clones and progenies (Table 19). In contrast to the Oregon tests, there was no association of maturity with seed yield and panicle production in the Iowa tests. As in the Oregon clonal test, girth was correlated with panicle number (r=0.78) but its correlation with seed yield was lower in Iowa (r=0.50) and similar to that between panicle number and seed yield (r=0.45). As was found for Oregon tests, high seed yield per panicle was associated with high seed number per panicle, high fertility index, and high 100-seed weight for both clones and progenies. Earlier-maturing plants in Iowa tended to have higher seed

Table 19. Phenotypic correlations among traits determined in Iowa seed yield experiments, 1982[a]

Trait	Seed yield	Panicle number	Seed yield/ panicle	No. seeds/ panicle	Panicle length	Fert. index	100-seed weight	Anthesis date	Plant height	Girth
Seed yield		0.45*	0.68**	0.54**	-0.26	0.47*	0.33	-0.29	0.02	0.50**
Panicle number	0.43*		-0.08	0.22	-0.11	-0.01	0.42*	0.03	0.13	0.78**
Seed yield/panicle	0.52**	-0.09		0.81**	-0.25	0.74**	0.45*	-0.49**	-0.36	0.12
No. seeds/panicle	0.72**	0.26	0.89**		0.07	0.37	-0.12	0.04	-0.01	0.30
Panicle length	-0.11	0.11	0.00	0.15		-0.39*	0.00	0.37	0.38*	0.17
Fertility index	0.35	-0.27	0.77**	0.66**	-0.38*		0.56**	-0.73**	-0.35	-0.03
100-seed weight	-0.14	-0.43*	0.42*	-0.03	-0.12	0.37		-0.67**	-0.30	0.08
Anthesis date	-0.11	0.24	-0.49**	-0.09	0.53**	-0.68**	-0.55**		0.63**	0.12
Plant height	0.18	0.42*	-0.33	-0.07	0.42*	-0.53**	-0.47*	0.77**		0.06
Lodging Score[b]	-0.40*	-0.50**	0.21	-0.13	-0.21	0.43*	0.55**	-0.50**	-0.67**	--

[a]Parent clone and progeny correlations are above and below diagonal line, respectively.

[b]Rated from 1=little to 5=severe lodging.

*,**Significant at the 5 and 1% levels, respectively.

yield per panicle, fertility index, and 100-seed weight for both clones and progenies. In 1982, a significant positive correlation of 0.45 between seed yield per panicle and 100-seed weight was obtained in the Iowa clonal test, while no association was found between those two traits in 1983 (Tables 19 and 20). In contrast to the Oregon tests, where plants with long panicles produced higher seed yields and heavier panicles, no association was found between panicle length and seed yield or between panicle length and seed yield per panicle in Iowa. In addition, plants with long panicles tended to be taller and have lower fertility index for both Iowa clones and progenies. Lodging tended to be associated with low seed yield, low panicle number, high fertility index, high 100-seed weight, early maturity, and short plants.

Prediction of Oregon seed yield

Oregon progeny seed yield (PSY) was significantly correlated in a positive manner with seed yield in the Oregon clonal test and Iowa progeny test; however, the correlation with Iowa progeny yield was of low predictive value (Table 21). No correlation was found between Oregon PSY and panicle number. High Oregon PSY was associated with high fertility index, high 100-seed weight, and early maturity in Oregon and Iowa clonal tests and the Iowa progeny test. The correlations were highest with anthesis date, ranging from -0.61 to -0.71. High Oregon PSY also tended to be associated with short plants in Iowa tests and tall plants in the Oregon clonal test. Oregon PSY was correlated positively with seed yield per panicle in the Oregon clonal and Iowa progeny

Table 20. Phenotypic correlations among traits determined in Iowa seed yield experiments, 1983[a]

Trait	Seed yield	Seed yield/ panicle	Fertility index	100-seed weight	Anthesis date
Seed yield		0.60**	0.44*	0.06	0.25
Seed yield/panicle	--		0.71**	0.21	0.21
Fertility index	--	--		0.42*	-0.14
100-seed weight	--	--	--		-0.64**
Anthesis date	-0.13	--	--	--	

[a]Parent clone and progeny correlations are above and below diagonal line, respectively.

*,**Significant at the 5 and 1% levels, respectively.

tests but not in the Iowa clonal test. High Oregon PSY was associated with long panicles only in the Oregon clonal test.

A summary of standardized partial regression coefficients from models with four and five variables for predicting Oregon PSY are presented in Table 22. Highest b values were obtained for anthesis date in models using clonal data and for seed yield per panicle in the model using Iowa progeny data. Negative b values were obtained for seed yield in models using Iowa data, indicating no relationship between Iowa and Oregon seed yield. Based on R^2 values, adding seed yield to the model results in only a 1 to 3% increase in precision of predicting Oregon seed yield. Multiple correlation coefficients of 0.73 and 0.81 were

Table 21. Correlations of Oregon progeny seed yield with traits determined in other seed yield tests

Trait	Seed yield tests		
	Oregon clonal	Iowa clonal	Iowa progenies
Seed yield	0.55**	0.04	0.38*
Panicle number	0.33	-0.29	-0.27
Seed yield/panicle	0.64**	0.32	0.67**
No. seeds/panicle	0.45*	0.15	0.41*
Panicle length	0.65*	0.10	0.13
Fertility index	0.56**	0.49**	0.47**
100-seed weight	0.38*	0.57**	0.61**
Anthesis date	-0.71**	-0.68**	-0.61**
Plant height	0.41*	-0.41*	-0.42*

*,**Significant at the 5 and 1% levels, respectively.

obtained for the models with five variables when Iowa clonal and progeny data were used, respectively.

The predicted genetic advance per cycle of selection was 85 kg/ha when selection was based on Oregon PSY (Table 23). Genetic advance decreased markedly when selection was based only on seed yield in other tests. Relative efficiencies were only 6 and 52% when selection was based on Iowa clonal and progeny seed yield, respectively. Selection for early maturity among clones in Iowa resulted in a predicted gain only 5 kg/ha less than selection for Oregon PSY itself. Similarly,

Table 22. Summary of standardized partial regression coefficients from models with four and five variables for predicting 1981-82 Oregon progeny seed yield from various tests

Independent variable	Oregon clonal test		Iowa clonal test		Iowa progeny test	
	Model I	Model II	Model I	Model II	Model I	Model II
Anthesis date	-0.5335	-0.5410	-0.5404	-0.5087	-0.3516	-0.3741
Seed yield/panicle	0.3928	0.3331	0.0777	0.2067	0.6873	0.8144
100-seed weight	0.0420	0.0411	0.1043	0.1278	0.2494	0.1775
Fertility index	-0.0114	-0.0615	0.0982	0.1025	-0.3810	-0.4124
Seed yield	--	0.1256	--	-0.2134	--	-0.1650
R	0.80	0.81	0.71	0.73	0.79	0.81
R^2	0.64	0.65	0.50	0.53	0.63	0.65

selection among clones in Iowa for early maturity, high 100-seed weight, high fertility index, and high seed yield per panicle by using the Smith-Hazel index was nearly as efficient as selection for Oregon PSY itself.

Forage Yield Test

Performance of Iowa breeding material

The performance of PC progenies, populations, and synthetics for traits determined in the PFY test in Iowa is summarized in Table 24. The population (76-OGP), synthetic (76-OGP-DT), and the average of the 27 PC progenies derived from the medium- to -early-maturity germplasm pool were superior in disease resistance, forage yield, and *in vitro* dry matter

Table 23. Predicted genetic advance in Oregon progeny seed yield when selection was based on various traits[a]

Selection criteria[b]	Predicted gain (kg/ha)	Relative efficiency (%)[c]
Oregon progeny seed yield	85	100
Oregon clonal seed yield	64	75
Iowa progeny seed yield	44	51.8
Iowa clonal seed yield	5	5.9
Iowa clonal test:		
Early maturity	80	94.1
High 100-seed weight	66	77.6
High fertility index	57	67.1
High seed yield per panicle	37	43.5
Smith-Hazel index[d]	83	97.6

[a]Selection intensity of 20%.

[b]All selection criteria based on two years data.

[c]Expressed as a percentage of the gain predicted for Oregon progeny seed yield.

[d]Selection for early maturity, high 100-seed weight, fertility index, and seed yield per panicle among Iowa clones.

Table 24. Mean performance of polycross progenies, populations, and synthetics traits determined in progeny forage yield test

Material	1981-83 Average days to heading past April 30	1981-82 Panicle number rating[a]	1982 Rust rating 9-22-82[b]	1981-82 Leaf disease rating[c]
75-OGP	21.3	3.1	2.1	2.0
76-OGP-DT	25.2	2.6	2.1	1.6
27 Polycross progenies				
Mean	25.2	2.8	2.0	1.7
Range	21.2-31.8	2.0-4.0	1.2-3.2	1.1-2.6
Sterling	18.5	4.6	4.4	4.5
C2-PR	18.6	4.2	2.9	2.8
C3-PG	18.6	4.3	3.2	2.3
Napier	19.7	4.3	3.8	3.1
Orion	34.0	1.7	2.2	1.4
Experiment mean	23.8	3.0	2.4	2.0
L.S.D. 0.05	1.8	0.5	0.3	0.5
C.V. %	8.1	9.6	2.4	6.7

[a]Rated from 1=few to 5=most panicles per plot.

[b]Rated from 1=resistant to 5=susceptible to rust.

[c]Rated from 1=least to 5=most diseased leaf area, average of 4 September 1981 and 8 June 1982 ratings.

Yield of dry matter (Mg/ha)				Average IVDMD (g/kg)	
1981	1982	1983	1981-83 Average	1981	1982
8.36	12.63	11.40	10.80	637	613
8.13	12.09	11.31	10.50	628	603
8.54	12.01	11.25	10.60	618	616
7.8-10.0	10.6-13.4	10.2-12.2	10.1-11.2	580-646	586-637
8.79	10.53	10.48	9.94	600	562
8.22	11.40	11.36	10.32	613	588
8.51	11.16	10.62	10.10	594	551
8.86	11.40	11.17	10.48	609	567
7.67	11.67	9.30	9.55	659	640
8.50	11.80	11.16	10.49	619	606
0.66	0.95	0.85	0.54	22	15
5.5	5.8	5.5	3.7	1.9	1.8

digestibility (IVDMD) to Sterling and the two synthetics derived from it. The 27 progenies averaged nearly the same as 76-OGP-DT in all traits. Only two progenies significantly exceeded 76-OGP-DT in forage yield over years (Table A10). C2-PR and C3-PG were superior in disease resistance and similar in forage yield to Sterling, the variety from which they were derived. The late-maturing, low-yielding variety Orion was highest in IVDMD.

Variability among polycross progenies

The performance of the 27 PC progenies in the PFY test is summarized in Tables A10 and A11. Analyses of variance for forage yield combined over harvests in 1981, 1982, and 1983 are presented in Table 25, and Table 26 gives analyses of variance for yearly total forage yield and yearly average IVDMD combined over years.

Significant differences ($P \leq 0.01$) were found among progenies in forage yield at each harvest in all three years, for 1981, 1982, and 1983 total yield, and for 1981-83 average annual yield. Interactions of entries with years and with harvests within years were significant (Tables 25 and 26). All progenies yielded more dry matter in 1982 than in 1981 and 1983 (Table A10). First harvests in 1981 and 1983 averaged lowest and highest in yield, respectively, among nine harvests. The low forage yield in 1981 can be attributed to extremely hot and dry weather during the spring of that year. PC progeny 35-16 was highest in total forage yield in 1981 with a yield of 9.95 Mg/ha, while PC progenies 30-15 and 39-12 topped the test in 1982 and 1983 with dry matter yields of 13.19 and 12.24 Mg/ha, respectively.

Table 25. Analyses of variance of forage yield data combined over harvests within years for 27 polycross progenies

Source of variation	df	Mean squares 1981	1982	1983
Replications (R)	3	0.5363	0.5950	0.7715
Entries (E)	26	0.2458**	0.4900**	0.2668**
Error (a)	78	0.0822	0.1763	0.1398
Harvests (H)	2	299.0799**	673.6075**	949.1767**
H x R	6	0.4211**	0.2672**	0.0148
H x E	52	0.0957**	0.6037**	0.1491**
Error (b)	156	0.0402	0.0578	0.0298

**Significant at the 1% level.

The range among PC progenies for heading date was 21.2 to 31.8 days past April 30. In the Iowa PSY test, a much narrower range among PC progenies for date of anthesis was observed (38.6-44.6) (Table 7).

Significant differences ($P \leq 0.01$) were found among progenies in IVDMD at each harvest in 1981 and 1982, for 1981 and 1982 yearly average IVDMD, and for 1981-82 average annual IVDMD. The entries by years interaction was significant for IVDMD (Table 26). PC progeny 03-08 averaged highest in IVDMD over years with a value of 640 g of digestible dry matter per kg of dry matter (Table A11). That progeny is characterized by later than average maturity, above average leaf disease resistance, average rust resistance, and well below average forage yield.

Table 26. Analyses of variance of forage yield and quality data combined over years for 27 polycross progenies

Source of variation	Yearly total forage yield (mg/ha)		Yearly average IVDMD (g/kg)	
	df	MS	df	MS
Replications (R)	3	0.9110	1	1779.25**
Entries (E)	26	1.2197**	26	1297.79**
Error (a)	78	0.5986	26	105.64
Years (Y)	2	358.7003**	1	252.35
Y x R	6	1.7537	1	1714.79**
Y x E	52	0.8895**	26	753.97**
Error (b)	156	0.2802	134	87.04

**Significant at the 1% level.

On the other hand, PC progeny 16-12 was lowest in IVDMD and characterized by being earlier than average in maturity, slightly above average in rust and leaf disease susceptibility, and above average in forage yield.

Estimates of variance components, narrow-sense heritabilities, and genetic and error CVs for traits determined in the PFY test are presented in Table 27. The variance component due to genotype by year interaction exceeded the corresponding genetic component of variance for forage yield, IVDMD, and leaf disease resistance. Narrow-sense heritability estimates were 0.41, 0.59, 0.90, and 0.45, for forage yield, IVDMD, rust and leaf disease resistance, respectively.

Table 27. Estimates of components of variance, narrow-sense heritabilities, and genetic and error coefficients of variation for traits determined in forage yield experiment

Character	$\hat{\sigma}^2_g$	$\hat{\sigma}^2_{gy}$	$\hat{\sigma}^2$	$\hat{h}^2$	Genetic CV	Error CV
1981-82 Average forage yield (Mg/ha)	0.052±0.030**	0.15±0.04**	0.28±0.03	0.41±0.22	2.2	7.3
1981-82 Average IVDMD (g/kg)	149.1±44.0**	166.8±50.0**	87.0±11.0	0.59±0.17	2.0	1.5
Rust resistance[a]	0.22±0.06**	--	0.09±0.01	0.90±0.25	23.0	15.0
Leaf disease resistance[b]	0.15±0.05**	0.338±0.10**	0.08±0.02	0.45±0.15	22.7	16.4

[a]Rated from 1=most resistance to 5=most susceptible on 22 September 1982.

[b]Rated from 1=least to 5=most diseased leaf area (average of ratings taken on 4 September 1981 and on 8 June 1982).

**Mean square associated with variance component significant at the 1% level.

Intercharacter correlations

Early-heading was associated with a large number of panicles at first harvest, low first-harvest and average IVDMD, and susceptibility to rust and leaf diseases (Table 28). Significant correlations of -0.73 and -0.57 between rust rating and 1982 third-harvest IVDMD and between leaf disease rating and 1982 first-harvest IVDMD, respectively, indicated the deleterious effects of disease on IVDMD. As expected, progenies which produced a greater number of panicles in spring tended to be lower in IVDMD at the time of first harvest.

Selection for Improved Seed and Forage Characteristics

Orchardgrass breeders must consider several traits when choosing among selection units. As the number of traits increases, the gain from selection for each individual trait will decrease. For example, if traits are uncorrelated and of equal importance, progress from selection for K traits by using index selection is only $1\sqrt{K}$ the progress based on selection for a single trait.

With this in mind, only four traits were included in a selection index as described by Smith (1936) and Hazel (1943). High Oregon progeny seed yield, high Iowa forage yield, high IVDMD, and rust resistance were considered equally important in development of an improved orchardgrass synthetic. Average annual forage yields and IVDMD were used rather than values for each individual harvest.

Knowledge of phenotypic and genotypic correlations among those selected seed and forage traits is necessary for calculation of the

Table 28. Correlations among traits determined in the forage yield test

Comparison			r Value
Heading date[a] vs. first-harvest dry matter yield			-0.13
Heading date vs. total dry matter yield			-0.30
Heading date vs. panicle number rating[b]			-0.68**
Heading date vs. average first-harvest IVDMD			0.66**
Heading date vs. average IVDMD over all harvests			0.64**
Heading date vs. rust rating 1982[c]			-0.46*
Heading date vs. leaf disease rating[d]		1981	-0.29
		1982	-0.64**
Rust rating vs. 1982 third-harvest IVDMD			-0.73**
Leaf disease rating vs. IVDMD:	third harvest	1981	-0.10
	first harvest	1982	-0.57**
Panicle number rating vs. first-harvest IVDMD		1981	-0.36
		1982	-0.42*
		1981-82	-0.60**
Panicle number rating vs. first-harvest dry matter yield 1981-82			0.29
Rust rating vs. 1982 third-harvest dry matter yield			0.01

[a]The number of days past April 30 when 50% of the panicles per plot were estimated to have emerged from the boot.

[b]Rated from 1=least to 5=most panicles per plot.

[c]Rated from 1=most resistant to 5=most susceptible to rust on 22 September 1982.

[d]Rated from 1=least to 5=most diseased leaf area on 4 September 1981 and on 8 June 1982.

*,**Significant at the 5 and 1% levels, respectively.

Smith-Hazel (SH) selection index. Only one significant phenotypic correlation of -0.59 existed among the four traits, and it was between IVDMD and rust resistance (Table 29). Oregon seed yield was not significantly correlated with Iowa forage yield, IVDMD, or rust rating. However, if we consider only first-harvest IVDMD and Oregon seed yield, then a significant correlation of -0.55 existed between the two traits. This probably reflects the correlation of 0.66 between IVDMD and maturity of the first harvest. No significant correlations were found between Iowa forage yield and IVDMD or rust rating. However, there was a tendency for progenies with high forage yield to be lower in IVDMD. Genotypic correlations were somewhat larger than phenotypic correlations.

Predicted gains from individual trait selection and from multiple trait selection, when the four traits were incorporated into a SH selection index, are presented in Table 30. The relative efficiency of index selection, compared to single trait selection, was 28, 30, 69, and 80%, respectively, for Oregon seed yield (OSY), Iowa forage yield (IFY), IVDMD, and rust resistance (RR). Predicted gains from a cycle of single trait selection were 85 kg/ha, 0.23 Mg/ha, 16 g/kg, and -0.5 rating points, respectively, for OSY, IFY, IVDMD, and RR, while predicted gains from multiple trait selection were 24 kg/ha, 0.07 Mg/ha, 11 g/kg, and -0.4 rating points, respectively, for OSY, IFY, IVDMD, and RR.

Correlated responses in other traits when selection was based on single traits are presented in Table 31. When selection was based on high OSY, the expected correlated changes in IFY, IVDMD, and RR were 0.16 Mg/ha, -6 g/kg, and 0.1 rating points, respectively. Changes in

Table 29. Correlations among selected seed and forage traits[a]

Character	Oregon progeny seed yield	Characters in Iowa forage test: Forage yield	IVDMD	Rust rating
1981-82 Average Oregon seed yield		0.36	-0.34	0.21
1981-83 Average Iowa forage yield	0.59		-0.18	0.20
1981-82 Average IVDMD	-0.41	-0.26		-0.59**
1982 Rust rating[b]	0.26	0.29	-0.64	

[a]Phenotypic and genotypic correlations are above and below diagonal line, respectively.

[b]Rated from 1=most resistance to 5=most susceptible on 22 September 1982.

**Significant at the 1% level.

a similar direction were obtained when selection was based on high IFY yield. However, when selection was based on high IVDMD, the expected correlated changes were -39 kg/ha, -0.08 Mg/ha, and -0.4 rating points, respectively, for OSY, IFY, and RR. Changes in a similar direction were obtained when selection was based on RR; predicted changes were -24 kg/ha, -0.09 Mg/ha, and 10 g/kg, respectively, for OSY, IFY, and IVDMD.

The mean performance of PC progenies when parent clones were selected on several bases are presented in Table 32. The five parent clones selected by the SH selection index were superior in average

Table 30. Comparison of predicted gains from individual trait selection (ΔG) with predicted gains from a Smith-Hazel (SH) selection index (ΔGSH) of all four traits[a]

Trait	b Values for SH	ΔG	ΔGSH	Relative efficiency of SH index[b]
1981-82 Average Oregon progeny seed yield (kg/ha)	.83	85	24	28
1981-83 Average Iowa forage yield (Mg/ha)	.50	0.23	0.07	30
1981-82 Average IVDMD (g/kg)	.98	16	11	69
1982 Rust rating[c]	-.64	-0.5	-0.4	80

[a]Selection intensity of 20%.

[b]Expressed as a percentage of the gain predicted by single-trait selection.

[c]Rated from 1=resistant to 5=susceptible.

performance for all traits when compared to clones selected on the basis of a single trait. However, selection of clones on the basis of a single trait resulted in the highest mean performance for that trait while performance for other traits was not maximized. The most dramatic decrease occurred for OSY and IFY when selection was based on high IVDMD or RR. Selecting parent clones on the basis of high IVDMD resulted in a mean progeny performance of 486 kg/ha and 10.39 Mg/ha for OSY and IFY, respectively, well below the average performance of all PC progenies for those two traits.

Table 31. Correlated response of traits when selection is based on a single trait

Selection criteria	ΔG[a]	Predicted gain from indirect selection: Oregon seed yield	Iowa forage yield	IVDMD	Rust resist.
1981-82 Average Oregon progeny seed yield (kg/ha)	85	--	0.16	-6	0.1
1981-83 Average Iowa forage yield (Mg/ha)	0.23	42	--	-3	0.1
1981-82 Average IVDMD (g/kg)	16	-39	-0.08	--	-0.4
1982 Rust rating[b]	-0.5	-24	-0.09	10	--

[a]Selection intensity of 20%.

[b]Rated from 1=resistant to 5=susceptible.

Table 32. Mean performance of polycross progenies when parent clones were selected for various traits[a]

Selection criterion	1981-82 Oregon progeny seed yield (kg/ha)	1981-83 Iowa forage yield (Mg/ha)	1981-82 Average IVDMD (g/kg)	1982 Rust rating[b]	Clones selected
Clones selected by SH index[c]	620	10.76	624	1.8	08-21,08-29,16-09, 18-21,31-09
1981-82 Average Oregon progeny seed production	661	10.70	611	2.2	10-27,12-12,16-09, 18-21,31-09
1981-83 Average Iowa forage production	567	11.04	611	2.4	12-12,18-28,30-15, 35-16,39-12
1981-1982 Average IVDMD	486	10.39	634	1.6	03-08,04-04,07-31, 08-21,08-29
1982 Rust rating	516	10.39	627	1.4	07-31,08-29,11-29, 27-16,31-09
Mean of progenies	553	10.60	617	2.0	
Sterling	658	9.94	581	4.4	

[a]Selection intensity of 20%.

[b]Rated from 1=most resistance to 5=most susceptible on 22 September 1982.

[c]Selection for high Oregon progeny seed yield, Iowa forage yield, IVDMD, and rust resistance.

DISCUSSION

Seed Yield

Results of this research indicated that orchardgrass breeding material selected primarily for forage traits in Iowa must undergo some selection for seed yield in the seed-producing area of Oregon. All of the Iowa-derived polycross (PC) progenies, populations, and synthetics yielded substantially less seed than Hallmark, a cultivar which was selected in part for seed production in Oregon. Eleven of the PC progenies, however, were similar in seed yield to Sterling, a cultivar which is acceptable for seed production in Oregon, indicating a synthetic could be formed from current breeding material which may be satisfactory in seed yield.

To assess the possibilities for genetic improvement of Oregon seed yield, it is necessary to have an understanding of the genetic variation, genotype by environment interactions, heritabilities, and interrelationships of seed production traits. My results indicated that selection for high polycross progeny seed yield in the seed producing area would be the most effective way of improving Oregon seed yield. Narrow-sense heritability estimates for progeny seed yield were 0.71 and 0.49 in Oregon and Iowa, respectively. Only the estimate based on Oregon data exceeded twice its standard error. Genotype by year components of variance were similar for both states, while the genotype component of variance for Oregon was more than three times that for Iowa. Although the genotype by year component of variance was smaller than the genotype component for Oregon progeny seed yield, it was of

sufficient magnitude to be of importance from the breeding viewpoint. Hence, it would be necessary to test progenies for more than one year to make progress from selection for high progeny seed yield.

A significant parent-progeny correlation of 0.55 indicated that selection among clones for seed yield in Oregon would result in some improvement in progeny seed yield in that state. Broad-sense heritability estimates indicated that greater progress could be made for improved clonal seed yield if selection was based on replicated material (0.31 and 0.67 in Oregon and 0.24 and 0.50 in Iowa on individual plant and entry mean bases, respectively). Significant genotype by year interactions for both Oregon and Iowa data again indicated the need for evaluating clonal seed yield for more than one year if progress from selection is to be expected. This is similar to the findings of Nguyen and Sleper (1983) who reported a significant genotype by year interaction variance component for clonal seed yield in tall fescue. Similarly, Bean (1972) reported larger genotype by year components of variance than genotype components for clonal seed yield in both tall fescue and timothy.

Evaluation of replicated clonal material, as opposed to polycross progenies, for seed yield offers several advantages from the breeding viewpoint. The length of time required for evaluation and selection of superior clones would be less. Clonal evaluation would also enable the breeder to screen more genotypes, thus allowing a greater selection intensity to be applied. Also, evaluation of a greater number of genotypes would allow the breeder the opportunity to select more individuals

to be recombined which would reduce undesirable effects of inbreeding and/or random drift which may occur when working with small populations.

Considering the components of seed yield, correlations obtained herein indicated that selection among clones in Oregon for high seed yield per panicle, long panicles, high fertility index, high 100-seed weight, and early maturity would result in some improvement in progeny seed yield. Frakes (1980) found that variation in clean seed weight per panicle accounted for a high proportion of the variation in seed yield per plant in tall fescue. Similarly, Dewey and Lu (1959) obtained a significant phenotypic correlation between seed weight per spike and seed yield per plant in crested wheatgrass. Reports in the literature are conflicting with regard to the association between panicle length and seed yield. Stoddert (1959) found that strains of timothy which had long panicles also produced higher seed yields. Jessen (1981), however, found no association between panicle length and seed yield in smooth bromegrass. Similarly, Bugge (1981) reported no correlation between long spikes and seed yield in perennial ryegrass.

Similar to the results presented herein, Leffel et al. (1954) obtained a positive association between cross-fertility and seed yields of parental orchardgrass clones. Similar results have been reported for other forage species (Lowe and Murphy, 1959; and Jessen, 1981). Stapledon (1928) found no association between bloom date and clonal seed yield in orchardgrass. Tomov and Blazhev (1975), on the other hand, examined orchardgrass clones of diverse origin and found that high seed yield was obtained mainly from early-maturing plants. Similar results have

been reported in other forage species (Stoddert, 1959; Christie and Kalton, 1960; and Nguyen and Sleper, 1983).

Evaluation of breeding material in the seed producing area is costly and not always possible. Therefore, the possibilities of improving Oregon seed production by selection on the basis of Iowa performance were of major interest. Large genotype by location interactions and nonsignificant or low correlations between locations for seed yield and panicle number of both clones and progenies indicated that selection for these traits in Iowa would be ineffective in terms of improving Oregon performance. Likewise, low and nonsignificant Iowa parent-Oregon progeny correlations for seed yield and panicle number indicated that selection among clones in Iowa would be ineffective for improvement of Oregon progeny performance for those traits. Panicle number in both the Iowa clonal and progeny tests was not correlated with progeny seed yield in Oregon. Although panicle number usually was correlated with seed yield within states, the low and nonsignificant correlations obtained herein between locations for panicle number probably were involved in the lack of association between panicle number in Iowa and progeny seed yield in Oregon. Bugge (1981) found that tiller production in Italian ryegrass was influenced largely by the environment. They reported no association between tiller number and seed yield. Similarly, Buckner et al. (1972) found no correlation between Prosser, Washington, and Lexington, Kentucky, for number of panicles per plant in tall fescue. They also reported a low relationship between number of panicles and seed yield.

Seed yield per panicle, the other major component of seed yield, was correlated significantly and positively with seed yield in all tests. A positive but not significant correlation of 0.32 was obtained between Iowa clonal seed yield per panicle and Oregon progeny seed yield. A significant Iowa parent-Oregon progeny correlation of 0.53 for seed yield per panicle indicated that selection among clones in Iowa would result in some improvement in Oregon performance. This correlation was similar in magnitude to the parent-progeny correlation of 0.57 based on Oregon data. A large genotype by year interaction and a nonsignificant correlation between years for seed yield per panicle of the clones in Iowa indicated that selection among clones in Iowa should be based on more than one year's results. In addition, a low broad-sense heritability of 0.24 on an individual plot basis for the clones in Iowa indicated that selection among individual plants would not be very effective. Previous findings also indicated that seed yield per panicle would be a useful selection criterion for seed yield. Anderson (1981) found that high seed yielding varieties of perennial ryegrass were characterized by high seed yield per ear, low shattering ability, and even ripeness. Similar results have been reported in other forage species (Frakes, 1980; and Dewey and Lu, 1959).

Fertility index, the estimate of relative seed set, was significantly correlated in a positive manner with seed yield of the clones but not the progenies in both states. The significant correlation of 0.49 between Iowa clonal fertility index and Oregon progeny seed yield indicated that fertility index offers some promise as a selection criterion

among clones in Iowa. Fertility index was always correlated significantly with seed yield per panicle (r-values ranged from 0.39 to 0.77). The Iowa parent-Oregon progeny correlation of 0.24 for fertility index was not significant; however, the parent-progeny correlation of 0.62 based on Iowa data was significant. Genotype and genotype by year components of variance and broad-sense heritabilities indicated that selection among clones in Iowa should be based on results from replicated trials conducted for more than one year. Leffel et al. (1954) found interannual correlations to be much lower for cross-fertility than self-fertility in orchardgrass, suggesting that factors affecting self-fertility were rather consistent in their reaction over years, while factors affecting open pollinated seed set were more subject to environmental influences. Similarly, Rincker et al. (1977) observed considerable variation among years in seed set of the six parent clones of "Vantage" reed canarygrass. Contrary to the results obtained herein, Ross and Adams (1955) found that seed set behavior in smooth bromegrass was largely independent of environmental influences and the variation observed in seed set among plants was largely due to additive gene action.

Seed weight and anthesis date also showed promise for use as selection criteria to improve Oregon seed yield. Among all traits studied in the Iowa clonal test, 100-seed weight and anthesis date showed the highest correlations (r=0.57 and -0.68, respectively) with Oregon progeny seed yield. Within tests, anthesis date was negatively correlated with seed yield in Oregon but not in Iowa, and seed weight was correlated with seed yield for only the progenies in Oregon. Seed weight and

anthesis date also showed the highest Iowa parent-Oregon progeny correlations (r=0.73 and 0.88, respectively). Relatively small genotype by location interactions and high correlations between locations for both clones and progenies also indicated that selection for these traits in Iowa would be effective in changing Oregon performance. Small genotype by year interactions and high correlations between years for these traits of the clones in Iowa indicated that selection among clones in Iowa could be based on one year's results. In addition, high broad-sense heritabilities of 0.90 and 0.84 on an individual plot basis for 100-seed weight and anthesis date, respectively, indicated that selection among individual plants would be effective. This would permit rapid evaluation of large populations and allow high selection intensity.

Panicle length did not seem to be useful as a selection criterion in Iowa for seed yield improvement in Oregon. Intercharacter correlations between panicle length and other traits related to seed yield were inconsistent. Long panicles tended to be associated with high seed yield per panicle and early maturity in Oregon but with low fertility index and late maturity in Iowa. This probably accounts for the fact panicle length was correlated with seed yield in Oregon but not in Iowa. Similar to the results of Nguyen and Sleper (1983), no significant association was found in this study between panicle length and 100-seed weight. Except for clones in Oregon, no association was found between panicle length and panicle number in either Oregon or Iowa.

The preceding discussion indicates that selection for greater seed yield per panicle, high fertility index, increased 100-seed weight,

and early maturity among clones in Iowa would result in some improvement in Oregon seed yield. In 1982 in the Iowa clonal test, these four traits were significantly correlated with each other in the following manner: greater seed yield per panicle with high fertility index, increased seed weight and early maturity, high fertility index with increased seed weight and early maturity, and increased seed weight with early maturity. Although three of these correlations were not significant in 1983, these associations do indicate that selection in Iowa for any one of the four traits would tend to give desired changes in the other three.

Selection among clones in Iowa for early maturity, increased seed weight, high fertility index, and greater seed yield per panicle by using the Smith-Hazel index was nearly as efficient as selection for Oregon progeny seed yield itself in terms of predicted genetic advance per cycle of selection. The predicted genetic advance in Oregon seed yield was 85 kg/ha when selection was based on Oregon progeny seed yield compared with 83 kg/ha when selection was based on the previously mentioned four traits determined on clones in Iowa. Similarly, selection among clones for only early maturity in Iowa resulted in a predicted gain only 5 kg/ha less than that based on selection for Oregon progeny seed yield itself. Nyugen and Sleper (1983) also concluded that increased seed yields in tall fescue could be expected from selection for early maturity. The results showing nearly as much predicted gain in Oregon seed yield from selection for early maturity among clones in Iowa as from direct selection for Oregon seed yield may seem unrealistic; however, since seed

yield is a complex character highly influenced by environmental variations, related characters with higher heritabilities, when properly weighted, may well serve as better indicators of the genetic yield potential of a progeny than seed yield itself. Similar results were obtained by Robinson et al. (1951) who showed a 14% advantage in predicted corn yield improvement when selection was based entirely on ears per plant compared with selection for yield itself.

The predicted genetic gains obtained herein may or may not be realized for several reasons. The true genotypic and phenotypic variances and covariances may change from those calculated for the 27 parent clones as cycles of selection are carried out. Since a 20% selection intensity allows for selection of only five parent clones, inbreeding depression and/or genetic drift may occur and predicted gains may not be realized. The Smith-Hazel index is considered optimum when accurate estimates of variances and covariances are available. Low standard errors were associated with genetic components of variance for anthesis date and 100-seed weight of the clones in Iowa; however, for seed yield per panicle and fertility index, genetic components of variance failed to exceed twice their standard errors.

Forage Characteristics

Material selected from the medium to early-maturing germplasm pool (EMGP) showed improvement in forage characteristics when compared with Sterling, Napier, and synthetics derived from Sterling. The population (75-OGP), synthetic (75-OGP-DT), and 27 polycross progenies derived from EMGP were superior in disease resistance, forage yield, and *in vitro* dry

matter digestibility (IVDMD) to Sterling and the two synthetics derived from it.

Intercharacter correlations revealed that early heading was associated with a large number of panicles at first harvest, low first-harvest and average IVDMD, and susceptibility to rust and leaf diseases. Christie and Mowat (1968) and Carlson (1974) also reported positive correlations between days to heading and IVDMD in orchardgrass. Similar to the findings of Carlson (1974), high IVDMD was associated with relatively few stems in the first harvest. Rust and other leaf diseases reduced IVDMD of susceptible entries. Significant correlations of -0.73 and -0.57 were obtained respectively between rust ratings and 1982 third-harvest IVDMD and between leaf disease ratings and 1982 first-harvest IVDMD. Carlson (1974) reported similar results. He found that leaf diseases, especially rust, reduced IVDMD values in orchardgrass.

Effect of Selection for Improved Seed Yield on Forage Yield and Quality

Associations between seed yield and the quantity and quality of the forage produced are important considerations in any forage breeding program. A positive but nonsignificant correlation of 0.36 between seed and forage yield indicated that forage yield would be maintained at high levels during selection for high seed yield. This is similar to the findings of Knowles et al. (1970) who reported no adverse effects on forage production from selection for improved seed yield in smooth bromegrass. Similarly, Kalton et al. (1955) obtained a low nonsignificant correlation of 0.16 between forage and seed yield of 20 orchardgrass

clones. Ross and Adams (1955) found no association between seed and forage yield of open-pollinated progenies of smooth bromegrass.

Correlations reported herein indicated a tendency for progenies exhibiting high seed yield in Oregon to be lower in IVDMD and more susceptible to rust in Iowa. A negative but nonsignificant correlation of -0.34 was obtained between seed yield in Oregon and IVDMD, while a nonsignificant r-value of 0.21 was obtained between Oregon seed yield and rust ratings. These relationships affected genetic gains. Negatively correlated responses in IVDMD from selection for Oregon seed yield and Iowa forage yield were obtained, indicating some compromises would be necessary when breeding for both forage and seed traits. Thus, in this material, IVDMD would be sacrificed to some extent if parent clones were selected only for high seed production in Oregon.

My results indicated that the S-H selection index would aid the breeder in identifying clones which are superior in average performance for several traits. Maximum single trait performance, however, would be sacrificed. Therefore, if individual trait superiority is desired, direct selection for the particular trait should be practiced.

The Smith-Hazel selection index presented herein may not be the best available index or even applicable in orchardgrass on a practical basis. It was presented to illustrate the usefulness of selection indexes. Since calculation of the Smith-Hazel index involves costly calculations of variances and covariances needed to assign relative economic weights, comparable gains may be possible by using other selection indexes with less cost per unit of progress. Several selection indexes are available to the plant breeder that are "weight-free"

(i.e., do not use relative weighting factors) or are "parameter free" (i.e., do not use genetic variances and covariances) (Elston, 1963; Mulamba and Mock, 1978; and Pesek and Baker, 1969).

As was demonstrated herein, the selection index does improve the plant breeders ability to select lines superior for more than one trait. The breeder, however, must be willing to set goals, and he must determine the relative importance of the traits needed to attain these goals.

SUMMARY

Orchardgrass clones, polycross (PC) progenies, synthetics, and populations selected for winter hardiness, disease resistance, and drought tolerance in Iowa were evaluated for seed yield and related traits near Corvallis, Oregon, and Ames, Iowa. Relationships between performance of parent clones and their PC progenies and between seed yield and other traits also were studied. Correlations between performances in the two states were of particular interest. In addition, the material in progeny seed yield tests also was evaluated for forage production and quality near Ames, Iowa. Relationships between seed and forage traits were studied.

None of the Iowa PC progenies, populations, and synthetics was superior in Oregon seed yield. The check variety Hallmark, selected in part for high seed yield in Oregon and the entry highest in that trait, yielded substantially more seed than any of the Iowa-derived PC progenies, cultivars, populations, and synthetics. It yielded 30% more seed than the highest yielding PC progeny and 43% more seed than Sterling, a cultivar selected for high seed yield in Iowa. Eleven of the PC progenies, however, were similar in seed yield to Sterling, a cultivar acceptable in Oregon seed production.

Large environmental differences between Corvallis, Oregon, and Ames, Iowa, resulted in significant differences between locations, large genotype by location interactions, and nonsignificant or low correlations between locations for seed yield and panicle number of both clones and

progenies. Average seed yields in Oregon were 39 and 51% greater than in Iowa for clones and progenies, respectively. Large genotype by location interactions and low correlations between locations also were obtained for seed yield per panicle and fertility index of the progenies and plant height of the clones.

Relatively small genotype by location interactions and high correlations between locations for anthesis date and 100-seed weight of both clones and progenies indicated that selection for these traits in Iowa would be effective in terms of changing Oregon performance.

In Oregon, large genotype by year interactions and low or nonsignificant correlations between years were obtained for seed yield per panicle, fertility index, and 100-seed weight of the progenies, and for number of seeds per panicle of the clones. Correlations between years ranging from 0.62 to 0.86 for seed yield, panicle number, panicle length, and anthesis date of both clones and progenies and for fertility index and plant height of the clones indicated greater reliability of one year's data in some instances. In contrast to Oregon results, a large genotype by year interaction was obtained for seed yield of both clones and progenies in Iowa. Interseasonal correlations in Iowa ranging from 0.87 to 0.95 for anthesis date of both clones and progenies and 100-seed weight of the clones indicated consistent year-to-year performance in these instances.

Heritability estimates calculated from components of variance were high for anthesis date of both clones and progenies. Values for seed

yield were higher for Oregon than Iowa experiments for both clones and progenies. Considering components of seed yield, heritability estimates were higher for panicle number than for seed yield per panicle. Consistently high values also were obtained for panicle length and for plant height, except for Oregon progenies.

Significant parent-progeny correlations were obtained for panicle length, 100-seed weight, and anthesis date in both states, seed yield and seed yield per panicle in Oregon, and fertility index and plant height in Iowa. R-values were highest for panicle length, 100-seed weight, and anthesis date, ranging from 0.76 to 0.89. Significant Iowa parent-Oregon progeny correlations were obtained for seed yield per panicle, panicle length, 100-seed weight, anthesis date, and plant height. Relatively high values of 0.73 and 0.88 were obtained for seed weight and anthesis date.

Intercharacter correlations revealed that high seed yield in Oregon was associated with high seed yield per panicle, long panicles, and early maturity of both clones and progenies. High seed yield in Iowa was significantly correlated with high panicle number, high seed yield per panicle, and high seed number per panicle. In contrast to Oregon results, there were no significant associations of maturity with seed yield and panicle production or of panicle length with seed yield per panicle in Iowa data. Intercharacter correlations between states revealed that Oregon progeny seed yield was significantly correlated with fertility index, 100-seed weight, anthesis date, and plant height of both clones and progenies in Iowa.

Greatest predicted genetic gains in Oregon progeny seed yield were obtained when selection was based on Oregon progeny seed yield; however, selection among clones in Iowa for early maturity or for a combination of early maturity, high seed yield per panicle, high fertility index, and high 100-seed weight by using the Smith-Hazel selection index gave predicted gains only 6 and 2% less, respectively, than those based on Oregon progeny seed yield.

Material selected from the medium- to early-maturing germplasm pool (EMGP) showed improvement in forage characteristics when compared with Sterling, Napier, and synthetics derived from Sterling. 75-OGP, 76-OGP-DT, and the 27 polycross progenies on the average were superior in disease resistance, forage yield, and in vitro dry matter digestibility (IVDMD) to Sterling and the two synthetics derived from it. The 27 PC progenies were 7 and 6% higher than Sterling in 1981-83 average forage yield and 1981-82 average IVDMD, respectively.

Large genotype by year interactions were obtained for forage yield, IVDMD, and leaf disease resistance. Heritability estimates calculated from components of variance were highest for rust resistance.

Intercharacter correlations revealed that early heading was associated with a large number of panicles at first harvest, low first-harvest and average IVDMD, and susceptibility to rust and other leaf diseases. In addition, correlations indicated deleterious effects of rust and other leaf diseases on IVDMD and forage yield. On 22 September 1982, the average yield and IVDMD were, respectively, 2.08 Mg/ha and 609 g/kg for the progenies compared with 0.61 Mg/ha and 508 g/kg for rust-susceptible Sterling.

Although not significant, high Oregon progeny seed yield tended to be associated with high forage yield and low IVDMD, indicating some compromise would be necessary when breeding for both forage and seed traits in this material. The Smith-Hazel index selection for high Oregon seed yield, Iowa forage yield, IVDMD, and rust resistance gave predicted improvement in all four traits, whereas selection for each trait singly did not. Single trait selection, however, gave the greatest predicted improvement in that trait. Selection for just Oregon progeny seed yield gave small, negatively correlated predicted responses in IVDMD and rust resistance.

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APPENDIX

Table A1. Performance of polycross progenies in a seed yield test conducted near Corvallis, Oregon

Polycross progeny	Trait determined											
	Seed yield (kg/ha)			Panicle number[a]			Seed yield/panicle (mg)			No. seeds/panicle		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82
01-30	355	741	548	266	214	240	223	613	418	274	777	526
03-08	248	495	372	242	208	225	306	533	419	378	614	496
04-04	241	500	371	179	176	178	261	567	414	312	721	517
05-02	262	853	557	295	274	285	173	551	362	235	508	372
07-31	301	804	553	247	170	208	222	622	422	340	746	543
08-21	420	719	569	216	175	196	323	691	507	449	738	594
08-29	347	784	565	253	214	233	245	710	478	262	719	490
09-21	287	738	513	262	246	254	233	533	383	296	728	512
10-27	465	978	722	261	264	262	282	642	462	319	695	507
10-32	252	547	400	219	232	225	204	590	397	244	881	563
11-29	307	634	470	255	229	242	237	529	383	295	704	499
12-12	406	831	618	261	213	237	223	636	429	296	654	475
16-09	426	848	637	283	227	255	223	717	470	259	634	447
16-12	344	784	564	286	226	256	227	621	424	306	618	462
18-21	464	908	686	274	244	259	288	642	465	314	790	552
18-28	453	755	604	234	165	200	326	604	465	458	637	548
22-21	325	783	554	309	276	293	209	565	387	296	691	494
27-16	305	806	555	220	196	208	231	656	444	332	763	548
30-15	332	767	549	244	204	224	221	593	407	361	858	610
31-09	454	826	640	248	201	225	286	561	424	392	585	489
32-02	441	791	616	241	238	240	312	639	475	409	700	555
33-02	329	813	571	266	257	262	205	668	437	323	710	516
35-16	352	704	528	263	203	233	244	736	490	303	821	562
35-22	371	805	588	242	240	241	242	616	429	285	646	465

[a]The number of panicles in a 0.914 meter sample of row.

Table A1. Continued

Polycross progeny	Trait determined											
	Seed yield (kg/ha)			Panicle number[a]			Seed yield/panicle (mg)			No. seeds/panicle		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82
39-12	291	785	538	297	291	294	173	530	352	273	566	419
40-12	324	815	570	255	284	270	245	539	392	332	609	471
40-23	254	745	499	303	224	263	137	528	333	193	553	373
Progeny mean	345	761	553	256	226	241	241	609	425	316	692	504
L.S.D., 0.05	64	166	125	30.3	55	38	72	113	ns[b]	ns	ns	ns
C.V. %	16.4	19.3	17.1	10.4	15.0	14.1	26.6	16.9	19.0	24.8	16.6	19.6

[b] ns=Nonsignificant at the 5% level.

Table A2. Performance of polycross progenies in a seed yield test conducted near Corvallis, Oregon

Polycross progeny	Trait determined: Panicle length (cm)			Fertility index (g/kg)			100-Seed weight (mg)			Anthesis date[a]			Plant height (cm)		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	81	82	81-82
01-30	16.2	20.1	18.2	395	632	514	63.7	85.9	74.8	28.5	33.8	31.2	165	131	148
03-08	16.8	20.6	18.7	420	555	488	76.8	75.2	76.0	31.2	40.5	35.8	160	124	142
04-04	15.1	19.1	17.1	429	633	531	91.7	82.2	87.0	34.3	39.5	36.9	157	132	145
05-02	15.8	20.2	18.0	357	617	487	71.5	93.1	82.3	26.5	31.3	28.9	160	131	146
07-31	17.0	21.1	19.1	413	651	532	63.5	94.0	78.8	29.3	34.0	31.7	159	131	145
08-21	16.6	22.2	19.4	518	628	573	76.2	84.8	80.5	29.3	35.5	32.4	160	135	148
08-29	17.3	21.8	19.5	383	642	513	85.4	93.6	89.5	29.0	31.3	30.2	161	136	148
09-21	16.7	20.7	18.7	440	599	520	70.2	78.5	74.4	29.7	35.5	32.6	157	129	143
10-27	18.7	20.4	19.6	474	631	552	78.8	93.2	86.0	27.5	32.5	30.0	153	124	138
10-32	14.0	19.7	16.8	397	615	506	76.6	68.0	72.2	38.0	41.0	39.5	161	128	144
11-29	13.5	20.2	16.8	458	610	534	71.3	75.0	73.2	30.0	38.5	34.1	162	135	148
12-12	16.1	21.5	18.8	450	672	561	76.0	99.5	87.8	28.5	32.0	30.2	160	130	145
16-09	18.8	23.6	21.2	406	667	537	69.2	94.8	82.0	28.5	33.0	30.8	152	138	145
16-12	17.4	20.1	18.7	384	623	503	75.2	96.2	85.6	27.5	32.0	29.8	148	124	136
18-21	17.6	22.9	20.3	466	628	547	75.8	85.9	80.8	27.5	32.0	29.8	154	132	143
18-28	18.2	20.9	19.6	459	625	542	92.4	92.6	92.5	28.5	33.0	30.8	153	124	138
22-21	17.3	21.9	19.6	434	652	543	67.4	85.1	76.2	29.3	33.0	31.2	151	132	142
27-16	16.2	20.7	18.5	390	635	512	60.8	90.4	75.6	28.0	34.0	31.0	165	134	149
30-15	18.4	22.5	20.5	384	589	486	71.6	77.8	74.6	28.5	33.5	31.0	163	136	150
31-09	19.0	23.4	21.2	436	589	513	81.9	83.8	82.9	28.5	34.5	31.5	162	138	150
32-02	18.0	24.9	21.5	468	566	517	90.9	91.4	91.1	30.0	35.0	32.3	161	135	148
33-02	17.4	21.1	19.3	389	658	523	76.1	89.4	82.8	28.5	32.0	30.2	147	122	135
35-16	16.3	21.9	19.1	400	645	522	82.7	104.4	93.5	28.5	32.0	30.2	149	131	140
35-22	18.9	22.0	20.4	412	590	501	80.9	87.2	84.1	28.0	32.5	30.2	162	141	151

[a]The number of days past April 30.

Table A2. Continued

Polycross progeny	Trait determined: Panicle length (cm)			Fertility index (g/kg)			100-Seed weight (mg)			Anthesis date[a]			Plant height (cm)		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	81	82	81-82
39-12	16.5	20.0	18.2	350	600	475	64.4	86.1	75.2	27.5	32.0	29.8	149	130	140
40-12	17.1	21.2	19.1	393	579	486	76.9	78.0	77.5	29.3	37.5	33.4	163	134	149
40-23	16.4	19.1	17.8	300	612	456	68.3	92.2	80.2	27.5	35.5	31.5	149	134	141
Progeny mean	16.9	21.2	19.1	415	620	518	75.4	87.3	81.4	29.1	34.3	31.7	157	131	144
L.S.D., 0.05	2.0	1.8	1.8	67	41	ns[b]	12.4	11.0	ns	2.6	2.4	2.5	72	8	8
C.V. %	10.6	7.6	8.9	14.4	5.9	9.6	8.0	6.1	7.0	7.9	6.3	7.0	4.2	5.5	4.9

[b]ns=Nonsignificant at the 5% level.

Table A3. Performance of polycross progenies in a seed yield test conducted near Ames, Iowa

Polycross progeny	Seed yield (kg/ha)			Antheses date[a]		
	1982	1983	82-83	1982	1983	82-83
01-30	444	385	415	38.8	44.0	41.4
03-08	336	288	312	43.5	45.8	44.6
04-04	331	198	264	43.2	45.5	44.4
05-02	437	333	385	39.0	43.8	41.4
07-31	340	276	308	38.8	45.0	41.9
08-21	515	379	447	41.0	44.0	42.5
08-29	392	330	361	37.0	43.2	40.1
09-21	439	285	362	42.0	44.8	43.4
10-27	366	330	348	37.8	42.8	40.3
10-32	403	283	343	42.0	45.8	43.9
11-29	443	260	352	42.0	44.5	43.2
12-12	580	352	466	38.0	42.8	40.4
16-09	346	339	342	39.0	43.2	41.1
16-12	286	334	310	38.2	42.5	40.4
18-21	448	396	422	38.8	43.0	40.9
18-28	481	370	426	39.0	43.5	41.2
22-21	372	249	310	37.8	43.2	40.5
27-16	556	374	465	39.8	44.2	42.0
30-15	446	271	358	41.2	44.2	42.8
31-09	397	363	380	40.5	44.5	42.5
32-02	332	417	375	41.2	44.5	42.9
33-02	355	320	338	39.2	43.0	41.2
35-16	463	389	426	37.0	43.0	40.0
35-22	365	270	318	37.8	43.0	40.4
39-12	432	205	318	36.0	41.2	38.6
40-12	387	284	336	39.5	44.2	41.9
40-23	415	365	390	39.0	43.5	41.2
Progeny mean	411	320	366	39.5	43.8	41.7
L.S.D., 0.05	113	53	109	1.6	0.8	1.7
C.V. %	19.5	11.9	17.1	2.8	1.3	2.1

[a]The number of days past April 30.

[b]The number of panicles in a 0.914 meter sample of row.

[c]Rated from 1=little to 5=severe lodging.

[d]ns=Nonsignificant at the 5% level.

Trait determined							
Panicle number[b]	Seed yield/ panicle (mg)	No. seeds/ panicle	Panicle length (cm)	Fertility index (g/kg)	100-Seed weight (mg)	Plant height (cm)	Lodging score[c]
286	346	367	15.6	573	97.4	114	1.4
286	251	315	17.7	446	83.4	114	1.8
223	253	272	15.5	480	98.0	120	1.0
290	343	345	15.3	580	92.4	112	1.6
256	338	313	16.1	546	87.4	112	1.5
300	410	450	15.8	562	95.8	119	1.2
218	338	270	14.1	597	110.0	111	2.1
274	335	321	17.1	535	88.6	116	1.2
222	389	421	15.2	614	107.0	102	2.8
320	295	334	15.5	478	87.0	119	1.2
239	358	340	15.5	568	91.8	117	1.4
262	430	420	15.1	613	108.8	112	2.0
250	416	362	16.5	616	111.9	115	3.8
212	364	279	13.7	606	110.8	101	4.2
252	505	453	18.0	631	106.3	107	2.2
320	392	365	16.4	527	112.2	111	1.5
226	418	445	16.4	639	107.2	108	2.4
264	420	432	14.9	603	91.0	115	1.6
260	377	460	16.7	591	93.7	116	1.5
197	404	423	18.0	568	103.6	111	2.5
236	283	270	17.9	473	105.6	114	3.4
232	340	300	15.0	511	110.0	107	2.2
254	383	359	14.4	615	110.8	104	2.1
270	324	285	15.6	517	111.8	108	2.4
234	363	358	13.6	646	97.0	99	3.8
234	365	327	15.7	484	102.0	111	1.5
262	406	345	14.3	636	103.9	105	3.0
255	365	357	15.8	565	100.9	111	2.1
51	100	ns[d]	1.4	71	14.0	4	0.8
14.1	19.0	19.6	6.0	8.8	6.7	3.4	26.7

Table A4. Performance of parent clones in a clonal seed yield test conducted near Corvallis, Oregon

Parent clone	Trait determined: Seed yield (g/plant)			Panicles/plant			Seed yield/panicle (mg)			No. seeds/panicle			Panicle length (cm)		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82
01-30	33.9	82.1	58.0	68	173	121	513	739	626	640	836	738	14.4	17.9	16.2
03-08	19.8	7.8	13.8	46	62	54	436	497	466	567	567	567	14.5	17.0	15.7
04-04	3.9	13.2	8.6	25	46	35	319	381	340	280	537	409	13.0	13.0	13.0
05-02	17.1	11.8	14.4	51	42	46	354	413	384	395	453	424	13.9	14.9	14.4
07-31	25.9	39.0	32.4	56	79	68	462	764	613	624	1063	844	12.7	18.0	15.4
08-21	21.2	37.4	29.3	37	66	52	618	605	612	611	518	565	16.6	16.9	16.7
08-29	31.3	107.1	69.2	51	123	87	491	1151	820	561	1055	808	14.8	25.6	20.2
09-21	17.8	18.4	18.1	60	68	64	381	478	430	376	762	569	14.0	17.4	15.7
10-27	16.9	25.7	21.3	31	30	31	521	978	750	735	857	796	16.6	17.9	17.3
10-32	7.6	10.3	9.0	23	31	27	405	300	352	618	441	529	10.4	9.2	9.8
11-29	25.4	34.6	30.0	70	131	100	460	725	592	774	872	823	12.8	17.4	15.1
12-12	39.7	86.6	63.2	73	140	106	733	845	789	799	759	779	17.4	18.8	18.1
16-09	49.6	64.8	57.2	81	138	109	534	753	644	543	810	676	15.5	18.3	16.9
16-12	31.1	64.2	47.6	59	159	109	667	830	748	792	861	827	15.5	16.4	15.9
18-21	40.7	111.8	76.2	74	197	136	810	921	866	844	1010	927	21.0	25.3	23.2
18-28	16.9	47.0	32.0	44	57	50	532	1081	806	537	1048	792	17.0	21.5	19.3
22-21	35.4	96.4	65.9	83	214	148	489	625	557	713	896	804	16.6	21.7	19.1
27-16	28.2	56.4	42.3	40	80	60	828	1122	974	1015	1360	1188	16.1	18.5	17.3
30-15	12.8	29.1	20.9	34	34	34	411	1081	746	524	1519	1021	18.8	22.6	20.7
31-09	41.6	109.5	75.6	68	178	123	696	784	740	694	1101	898	21.8	27.6	24.7
32-02	27.3	64.2	45.8	53	132	93	516	791	654	376	824	600	16.0	26.6	21.3
33-02	31.2	55.9	43.6	62	134	98	789	520	654	999	390	695	18.1	14.7	16.4
35-16	19.2	29.9	24.6	37	92	65	637	736	687	583	697	640	15.0	16.1	15.6
35-22	19.6	27.6	23.6	49	52	51	558	878	718	463	1011	737	20.6	18.6	19.6
39-12	13.2	39.0	26.1	55	91	73	278	572	425	440	737	589	14.8	16.8	15.8

Table A4. Continued

Parent clone	Trait determined: Seed yield (g/plant) 1981	1982	81-82	Panicles/plant 1981	1982	81-82	Seed yield/panicle (mg) 1981	1982	81-82	No. seeds/panicle 1981	1982	81-82	Panicle length (cm) 1981	1982	81-82
40-12	14.8	18.0	16.4	50	45	47	312	625	468	497	947	722	12.6	15.3	14.0
40-23	21.9	52.2	37.0	58	119	88	390	774	582	406	723	565	16.0	17.7	16.8
Parental means	24.6	49.6	37.1	53	100	77	524	740	632	608	839	723	15.8	18.6	17.2
L.S.D., 0.05	12.7	36.4	34.5	21	69	61	170	360	310	305	572	ns[a]	3.2	4.8	4.6
C.V. %	41.2	58.4	58.2	52.2	55.0	52.8	26.7	38.7	35.4	24.3	33.1	30.7	16.4	20.5	18.9

[a]ns=Nonsignificant at the 5% level.

Table A5. Performance of parent clones in a clonal seed yield test conducted near Corvallis, Oregon

Parent clone	Trait determined: Fertility index (g/kg)			100-Seed weight (mg)			Anthesis date[a]			Plant height (cm)			Girth (cm)		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82
01-30	558	673	616	73.2	85.8	79.5	36.6	30.4	33.5	136	116	126	10.0	19.5	14.8
03-08	384	436	410	84.8	74.0	79.4	49.8	46.4	48.1	104	90	97	8.3	11.7	10.0
04-04	357	516	437	109.8	82.6	96.2	45.8	44.2	45.0	96	76	86	6.9	10.9	8.9
05-02	673	637	655	85.8	96.2	91.0	28.2	26.8	27.5	119	73	96	6.4	8.0	7.2
07-31	571	654	613	81.6	88.5	85.0	40.2	32.0	36.1	119	92	106	7.7	13.4	10.6
08-21	466	496	481	98.5	73.0	85.8	42.0	35.8	38.9	121	94	108	8.1	11.8	9.9
08-29	507	655	581	94.6	107.2	100.9	33.8	30.4	32.1	125	118	122	9.5	18.4	13.9
09-21	490	524	507	71.8	72.6	72.2	42.0	35.6	38.8	110	77	94	8.7	12.2	10.5
10-27	536	713	625	80.0	100.5	90.2	24.8	30.6	27.7	107	76	92	6.7	7.0	6.9
10-32	506	475	491	76.3	61.0	68.6	46.8	46.2	46.5	100	69	84	5.1	5.9	5.5
11-29	483	617	550	64.8	72.2	68.5	36.2	41.0	38.6	116	103	110	8.8	15.7	12.3
12-12	645	737	691	95.5	115.8	105.7	30.6	29.6	30.1	126	108	117	9.4	15.6	12.5
16-09	658	745	702	83.0	103.6	93.3	30.8	31.2	31.0	131	102	116	10.9	14.5	12.7
16-12	651	686	669	97.1	115.4	106.2	28.2	25.2	26.7	120	92	106	8.7	16.0	12.3
18-21	589	654	621	81.3	83.6	82.5	27.8	27.2	27.5	127	116	122	10.1	18.7	14.4
18-28	481	570	525	98.1	130.5	114.3	36.6	30.6	33.6	101	74	88	8.3	11.5	9.9
22-21	676	706	691	92.4	84.2	88.3	29.0	29.6	29.3	126	112	119	9.8	17.5	13.6
27-16	618	629	624	93.5	92.9	93.2	38.8	35.8	37.3	127	109	118	8.8	13.8	11.3
30-15	466	663	564	61.4	71.6	66.6	33.6	28.2	30.9	105	81	93	7.4	9.8	8.6
31-09	534	585	559	89.0	91.6	90.4	31.2	29.6	30.4	146	109	128	10.4	22.0	16.2
32-02	512	569	540	122.4	95.0	108.7	40.6	32.6	36.6	121	98	110	8.7	19.5	14.1
33-02	628	653	640	106.2	89.0	97.6	28.8	31.2	30.0	114	89	102	8.3	14.0	11.2
35-16	621	673	647	102.4	95.9	99.2	30.4	30.8	30.6	128	95	112	7.5	13.5	10.5
35-22	470	595	533	103.6	103.4	103.5	27.8	25.6	26.7	114	89	102	10.3	10.9	10.6
39-12	538	653	596	72.2	76.6	74.4	28.2	25.6	26.9	116	86	101	7.1	12.4	9.7

[a]The number of days past April 30.

Table A5. Continued

Parent clone	Trait determined														
	Fertility index (g/kg)			100-Seed weight (mg)			Anthesis date[a]			Plant height (cm)			Girth (cm)		
	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82	1981	1982	81-82
40-12	475	622	549	78.2	91.7	84.9	37.8	35.6	36.7	109	90	100	6.8	9.0	7.9
40-23	566	712	639	73.6	104.6	89.1	28.6	25.6	27.1	114	95	104	6.9	11.4	9.2
Parental means	543	624	584	87.8	91.1	89.4	34.6	32.3	33.5	118	94	106	8.4	13.5	10.9
L.S.D., 0.05	86	103	88	18.2	21.2	19.5	4.4	4.9	5.0	12	19	13	2.2	5.8	4.4
C.V. %	12.6	13.2	13.6	10.0	11.3	10.7	10.0	12.0	11.0	8.5	16.2	12.0	21.0	34.2	31.8

Table A6. Performance of parent clones in a clonal seed yield test conducted near Ames, Iowa

Parent clone	Trait determined: Seed yield (g/plant)			Seed yield/panicle (mg)			Fertility index (g/kg)			100-Seed weight (mg)			Anthesis date[a]		
	1982	1983	82-83	1982	1983	82-83	82	83	82-83	1982	1983	82-83	1982	1983	82-83
01-30	37.4	24.6	31.0	400	254	327	599	526	463	85.0	81.1	83.0	40.0	44.2	42.1
03-08	34.8	30.3	32.6	402	237	319	451	303	377	67.6	65.0	66.3	46.8	50.2	48.5
04-04	15.5	13.5	14.5	223	305	263	407	412	409	81.4	77.7	79.6	46.2	51.0	48.6
05-02	37.1	19.0	28.0	338	117	228	631	407	519	110.2	95.1	102.6	38.2	43.2	40.7
07-31	40.3	14.7	27.5	413	285	349	545	461	503	75.4	72.1	73.7	41.4	46.6	44.0
08-21	42.0	37.0	39.5	477	403	440	555	501	528	96.4	96.4	96.4	39.0	45.2	42.1
08-29	52.8	28.5	40.7	566	437	502	637	577	607	116.3	106.6	111.4	36.2	42.4	39.3
09-21	16.1	8.9	12.5	225	173	199	376	365	371	61.8	61.2	61.5	43.8	46.9	45.4
10-27	14.1	9.4	11.8	496	207	351	600	412	506	104.9	89.0	97.0	34.8	42.0	38.4
10-32	26.0	29.2	27.6	410	342	376	514	487	500	65.7	61.6	63.7	46.0	51.0	48.5
11-29	27.7	7.2	17.4	337	191	264	457	410	433	64.2	61.7	63.0	42.2	45.8	44.0
12-12	62.6	21.3	42.0	724	241	483	731	482	607	111.0	106.2	108.6	36.6	42.0	39.3
16-09	18.5	10.2	14.4	341	129	235	606	--	--	105.2	91.5	98.4	40.8	43.4	42.1
16-12	28.8	15.1	22.0	566	305	435	717	564	640	109.4	111.6	111.5	33.6	40.8	37.2
18-21	33.3	20.4	26.8	492	263	377	638	491	565	90.4	81.4	85.9	37.0	42.2	39.6
18-28	35.4	16.1	25.7	359	223	291	476	450	463	132.3	130.8	131.6	37.6	43.0	40.3
22-21	39.4	10.2	24.8	474	139	307	667	--	--	105.6	100.0	102.8	38.0	42.5	40.2
27-16	40.1	35.5	37.8	426	363	394	569	532	550	85.1	83.8	84.8	42.0	44.6	43.3
30-15	57.1	18.5	37.8	668	220	444	713	454	584	101.4	102.3	101.9	37.8	42.0	39.9
31-09	17.9	15.4	16.7	582	406	494	634	507	570	110.5	92.8	101.7	40.8	43.6	42.2
32-02	34.4	37.5	35.9	472	425	449	531	488	509	107.3	102.7	105.0	39.8	44.8	41.9
33-02	49.9	17.0	33.4	782	325	554	672	518	595	112.5	107.1	109.8	37.0	42.0	39.5
35-16	29.4	16.9	23.1	448	354	401	675	481	578	108.5	98.7	103.6	36.2	41.8	39.0
35-22	54.9	9.6	32.2	588	333	461	562	422	492	107.8	104.8	106.3	37.8	43.2	40.5

[a]The number of days past April 30.

Table A6. Continued

Parent clone	Trait determined: Seed yield (g/plant) 1982	1983	82-83	Seed yield/panicle (mg) 1982	1983	82-83	Fertility index (g/kg) 82	83	82-83	100-Seed weight (mg) 1982	1983	82-83	Anthesis date[a] 1982	1983	82-83
39-12	30.3	7.6	18.8	418	33	226	660	147	404	88.0	77.8	82.7	33.4	40.0	36.7
40-12	35.3	14.8	25.1	384	283	333	546	394	470	91.6	83.2	87.4	39.6	46.2	42.9
40-23	21.1	21.6	21.3	300	188	244	530	491	511	106.8	89.9	98.4	36.8	42	39.4
Parental mean	34.5	18.9	26.7	456	266	361	582	451	517	96.4	90.2	93.2	39.2	44.2	41.7
L.S.D., 0.05	13.1	7.1	ns[b]	120	101	195	55	70	157	9.9	12.7	8.2	1.7	1.1	1.9
C.V. %	30.3	29.8	19.8	20.9	23.0	23.8	7.6	9.4	8.5	5.0	6.8	5.9	3.4	2.0	2.7

[b] ns=Nonsignificant at the 5% level.

Table A7. Performance of parent clones in a clonal seed yield test conducted near Ames, Iowa, 1982

Material	Panicles/ plant	No. seeds/ panicle	Panicle length (cm)	Plant height (cm)	Girth (cm)
01-30	149	479	17.7	144	11.9
03-08	171	631	21.6	140	14.7
04-04	129	268	18.7	144	12.3
05-02	166	352	17.1	141	11.3
07-31	141	585	19.5	142	12.1
08-21	111	501	19.1	144	12.1
08-29	136	493	18.2	136	11.7
09-21	102	322	21.0	136	10.2
10-27	51	496	18.8	120	7.9
10-32	87	463	16.8	138	9.6
11-29	173	721	18.9	134	12.8
12-12	150	710	18.2	141	12.4
16-09	126	385	20.3	134	11.3
16-12	116	433	14.1	113	11.2
18-21	152	622	20.6	126	12.4
18-28	147	275	18.4	125	12.8
22-21	112	454	22.1	138	12.3
27-16	117	574	17.0	134	12.0
30-15	144	643	16.5	131	13.7
31-09	55	588	21.8	136	8.6
32-02	119	502	23.2	125	13.8
33-02	119	791	15.6	119	11.8
35-16	122	381	14.8	124	9.7
35-22	134	548	17.5	122	12.1
39-12	156	378	16.3	118	13.2
40-12	107	423	16.1	132	9.2
40-23	102	281	19.3	137	8.8
Parental mean	126	493	18.5	132	11.6
L.S.D., 0.05	35	227	1.9	8	2.3
C.V. %	22.5	22.4	8.4	4.9	15.6

Table A8. Phenotypic correlations among traits determined in Oregon seed yield experiments 1981[a]

Trait	Seed yield	Panicle number	Seed yield/ panicle	No. seeds/ panicle	Panicle length	Fert. index	100-Seed weight	Anthesis date	Plant height	Girth
Seed yield		0.82**	0.64**	0.52**	0.46*	0.60**	0.10	-0.39*	0.81**	0.82**
Panicle number	0.01		0.27	0.28	0.30	0.55**	-0.12	-0.43*	0.63**	0.72**
Seed yield/panicle	0.60**	-0.56**		0.80**	0.61**	0.45*	0.39*	-0.30	0.53**	0.53**
No. seeds/panicle	0.49**	-0.50**	0.84**		0.30	0.47*	0.01	-0.26	0.36	0.30
Panicle length	0.67**	0.19	0.32	0.35		0.15	0.22	-0.54*	0.40*	0.57**
Fertility index	0.58**	-0.43*	0.82**	0.67**	0.12		0.05	-0.65**	0.59**	0.24
100-Seed weight	0.35	-0.47*	0.62**	0.43*	0.20	0.39*		0.04	0.08	0.18
Anthesis date	-0.39*	-0.60**	0.10	-0.01	-0.52**	0.14	0.26		-0.40*	-0.25
Plant height	-0.07	-0.51**	0.23	0.18	-0.19	0.20	-0.03	0.24		0.68**
Girth	--	--	--	--	--	--	--	--	--	

[a]Parent clone and progeny correlations are above and below diagonal line, respectively.

*,**Significant at the 5 and 1% levels, respectively.

Table A9. Phenotypic correlations among traits determined in Oregon seed yield experiments 1982[a]

Trait	Seed yield	Panicle number	Seed yield/ panicle	No. seeds/ panicle	Panicle length	Fert. index	100-Seed weight	Anthesis date	Plant height	Girth
Seed yield		0.87**	0.48**	0.34	0.72**	0.47*	0.34	-0.47*	0.84**	0.85**
Panicle number	0.37		0.16	0.10	0.51**	0.45*	0.16	-0.36	0.81**	0.88**
Seed yield/panicle	0.31	-0.31		0.81**	0.65**	0.46*	0.55**	-0.48**	0.42*	0.31
No. seeds/panicle	-0.22	-0.33	0.41*		0.62**	0.30	0.20	-0.33	0.34	0.27
Panicle length	0.40*	-0.04	0.46*	0.13		0.21	0.28	-0.43*	0.58**	0.70**
Fertility index	0.27	-0.17	0.57**	0.21	-0.08		0.49**	-0.72**	0.41*	0.25
100-Seed weight	0.54**	-0.13	0.60**	-0.23	0.19	0.55**		-0.54**	0.14	0.17
Anthesis date	-0.80**	-0.19	-0.47*	0.16	-0.31	-0.45*	-0.76**		-0.25	-0.27
Plant height	0.12	-0.07	0.10	0.02	0.48**	-0.11	-0.04	-0.05		0.84**
Girth	--	--	--	--	--	--	--	--	--	

[a]Parent clone and progeny correlations are above and below diagonal line, respectively.

*,**Significant at the 5 and 1% levels, respectively.

Table A10. Polycross progeny means for forage yield

Material	Yield of dry matter (mg/ha)												
	1981				1982				1983				81-83
	6-1	7-17	9-14	Total	6-10	7-22	9-22	Total	6-9	7-18	9-27	Total	average
01-30	1.85	2.30	4.79	8.95	6.10	3.00	1.93	11.03	7.15	2.12	1.85	11.11	10.36
03-08	1.32	2.07	4.59	7.98	7.58	2.67	1.73	11.97	7.11	1.88	1.47	10.46	10.14
04-04	1.45	2.11	4.85	8.41	7.12	2.76	2.28	12.16	6.51	2.28	1.44	10.23	10.26
05-02	1.76	2.16	4.64	8.55	7.40	2.98	2.04	12.43	7.57	2.14	1.49	11.20	10.73
07-31	1.40	2.15	4.60	8.15	6.24	3.28	1.82	11.34	7.03	2.30	1.58	10.91	10.13
08-21	1.83	2.17	4.90	8.90	7.12	2.88	2.41	12.42	7.29	2.05	1.70	11.04	10.79
08-29	1.85	2.16	4.77	8.79	6.26	3.18	2.29	11.73	7.29	2.40	1.74	11.42	10.65
09-21	1.38	2.04	5.00	8.41	7.33	2.83	2.03	12.19	7.37	2.14	1.52	11.03	10.54
10-27	1.80	2.04	4.77	8.61	5.33	3.15	2.11	10.60	7.39	2.17	1.77	11.32	10.18
10-32	1.28	2.04	4.91	8.23	7.34	2.88	2.04	12.26	7.18	2.02	1.58	10.79	10.43
11-29	1.36	1.98	4.44	7.77	6.74	3.07	1.90	11.71	7.16	2.50	1.42	11.08	10.19
12-12	1.60	2.25	5.10	8.95	6.87	3.25	2.03	12.15	7.82	2.05	1.84	11.70	10.93
16-09	1.88	2.25	4.80	8.93	6.52	3.17	2.20	11.89	7.69	2.05	2.02	11.77	10.86
16-12	1.59	2.23	4.49	8.31	7.01	3.43	2.06	12.50	7.43	2.24	1.76	11.43	10.74
18-21	1.48	2.18	4.64	8.29	6.69	3.44	2.41	12.54	7.31	2.44	1.83	11.58	10.80
18-28	1.77	2.19	5.12	9.08	6.83	3.16	2.16	12.15	7.61	2.06	1.93	11.59	10.94
22-21	1.65	2.08	4.53	8.27	5.82	3.26	2.18	11.27	7.43	2.31	1.88	11.61	10.38
27-16	1.64	2.25	4.61	8.50	7.25	2.88	1.91	12.03	7.69	2.32	1.66	11.66	10.73
30-15	1.65	1.98	4.72	8.35	8.13	3.07	2.18	13.38	7.01	2.21	1.70	10.91	10.88
31-09	1.68	2.40	4.52	8.60	6.97	3.06	2.20	12.24	7.15	2.09	2.06	11.30	10.71
32-02	1.42	2.22	4.74	8.38	7.37	2.98	1.97	12.33	7.13	1.92	1.79	10.84	10.51
33-02	1.53	2.00	4.49	8.01	6.64	2.98	2.08	11.70	7.63	2.14	1.89	11.66	10.46
35-16	2.03	2.63	5.28	9.95	6.94	3.09	2.18	12.21	7.39	1.92	2.21	11.52	11.23
35-22	1.69	2.23	4.79	8.71	6.54	3.23	2.25	12.02	7.43	2.20	1.83	11.46	10.73
39-12	1.66	2.14	4.50	8.30	7.32	3.48	2.39	13.19	7.63	2.58	2.03	12.24	11.24
40-12	1.60	2.14	5.01	8.75	6.66	3.15	1.95	11.77	7.10	2.30	1.88	11.28	10.60
40-23	1.97	2.06	4.54	8.57	6.27	3.07	1.78	11.12	7.04	2.08	1.51	10.63	10.10

Table A10. Continued

Material	Yield of dry matter (mg/ha)												
	1981				1982				1983				81-83
	6-1	7-17	9-14	Total	6-10	7-22	9-22	Total	6-9	7-18	9-27	Total	average
Progeny mean	1.63	2.17	4.74	8.54	6.83	3.09	2.09	12.01	7.32	2.18	1.75	11.25	10.60
L.S.D., 0.05	0.31	0.29	0.38	0.70	0.60	0.33	0.33	1.02	0.47	0.29	0.34	0.87	0.63
C.V. %	13.5	9.6	5.6	5.8	6.2	7.7	11.3	6.1	4.6	9.6	13.7	5.5	7.3

Table A11. Performance of polycross progenies in a forage yield test conducted near Ames, Iowa, 1981-83

Material	1981-83 Average days to heading past 4/30	1981-82 Panicle number rating[a]	1982 Rust rating 9-22-82[b]	1981-82 Leaf disease rating[c]	IVDMD (g/kg) 1981 6-1	7-17	9-14	Avg.	IVDMD (g/kg) 1982 6-10	7-22	9-22	Avg.	81-82 Avg.
01-30	25.6	3.4	2.0	2.0	623	704	612	646	569	646	625	614	630
03-08	31.2	2.2	2.1	1.3	630	664	644	646	631	659	610	633	640
04-04	31.2	2.0	1.2	1.6	639	648	634	640	609	659	613	627	634
05-02	27.2	2.8	2.0	1.7	582	698	583	621	572	640	623	612	616
07-31	27.8	2.2	1.5	1.7	605	672	612	630	650	624	637	637	633
08-21	26.7	2.6	1.8	1.2	639	694	586	640	610	655	621	629	634
08-29	22.4	3.1	1.4	1.3	612	676	649	646	620	629	598	616	631
09-21	28.4	2.3	1.6	1.6	609	680	577	622	625	652	614	630	626
10-27	21.7	3.2	2.5	2.5	535	642	588	588	564	642	596	601	595
10-32	31.8	2.1	2.3	1.2	607	653	577	612	599	633	599	610	611
11-29	27.3	2.4	1.4	1.1	626	633	551	603	637	639	620	632	618
12-12	23.9	3.2	2.5	1.4	614	651	564	610	591	631	586	602	606
16-09	25.8	3.1	2.1	1.9	594	712	583	630	596	642	605	614	622
16-12	22.6	3.0	2.2	1.9	556	643	542	580	579	637	604	606	593
18-21	24.9	2.9	2.3	2.4	576	688	588	617	594	636	623	618	618
18-28	26.5	3.0	2.7	1.6	622	697	594	638	594	637	598	610	624
22-21	24.9	2.6	2.1	2.4	592	702	605	633	592	628	605	608	621
27-16	27.5	2.6	1.5	1.4	586	652	575	604	614	657	637	636	620

[a]Rated from 1=least to 5=most panicles per plot.

[b]Rated from 1=resistant to 5=susceptible to rust.

[c]Rated from 1=least to 5=most diseased leaf area, average of 4 September 1981 and 8 June 1982 ratings.

Table A11. Continued

Material	1981-83 Average days to heading past 4/30	1981-82 Panicle number rating[a]	1982 Rust rating 9-22-82[b]	1981-82 Leaf disease rating[c]	IVDMD (g/kg) 1981 6-1	7-17	9-14	Avg.	IVDMD (g/kg) 1982 6-10	7-22	9-22	Avg.	81-82 Avg.
30-15	26.5	2.7	1.9	1.4	581	664	519	588	601	649	615	621	605
31-09	25.4	2.8	1.5	1.8	585	674	587	615	604	634	618	619	617
32-02	27.2	2.8	2.0	1.6	574	668	594	612	605	655	605	621	617
33-02	23.5	3.1	2.4	2.4	558	672	547	592	577	634	592	601	597
35-16	23.5	2.7	1.9	1.8	597	668	586	617	589	635	617	614	615
35-22	26.6	2.4	2.1	1.3	591	650	587	610	606	648	634	629	619
39-12	21.4	3.2	3.2	2.6	589	673	563	608	576	645	575	598	603
40-12	27.1	2.4	2.0	1.3	629	665	611	635	588	639	611	613	624
40-23	21.2	4.0	3.1	1.7	580	678	579	612	580	619	561	586	599
Progeny mean	25.2	2.8	2.0	1.7	597	671	587	618	599	641	609	616	617
L.S.D., 0.05	1.7	0.5	0.4	0.4	29	29	35	16	38	19	36	15	27
C.V. %	8.6	10.4	15.0	16.4	3.3	3.0	4.1	1.7	4.4	2.1	4.1	1.7	1.5